

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 9, 2003, 09:17:42 ; Search time 42 Seconds

(without alignments)
117.155 Million cell updates/sec

Title: US-09-835-107A-11

Perfect score: 175

Sequence: 1 KPVSLSYRCPGRFFGGGLKWTQYLEKALN 31

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues 1107863

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	175	100.0	31	23	AAB47686 SDF-1(1-14) - (G)4
2	175	100.0	31	23	AAB47693 SDF-1(1-14) - (G)4
3	175	100.0	31	23	AAB47695 SDF-1(1-14) - (G)4
4	175	100.0	31	23	AAB47700 SDF-1(1-14) - (G)4
5	175	100.0	31	23	AAB47701 SDF-1(1-14) - (G)4
6	175	100.0	31	23	AAB47702 SDF-1(1-14) - (G)4
7	175	100.0	31	23	AAB47703 SDF-1(1-14) - (G)4
8	175	100.0	31	23	AAB47706 SDF-1(1-14) - (G)4
9	175	100.0	31	23	AAB47707 SDF-1(1-14) - (G)4

10	175	100.0	31	23	AAB47714 SDF-1(1-14) - (G)4
11	175	100.0	31	23	AAB47715 SDF-1(1-14) - (G)4
12	175	100.0	31	23	AAB47716 SDF-1(1-14) - (G)4
13	175	100.0	31	23	AAB47717 SDF-1(1-14) - (G)4
14	172	98.3	31	23	AAB47704 SDF-1(1-14) - (G)4
15	172	98.3	31	23	AAB47705 SDF-1(1-14) - (G)4
16	167	95.4	31	21	AAB28545 Chemokine-derived
17	166	94.9	31	23	AAM48698 CXCR4 cyclic pepti
18	163.5	93.4	34	23	AAB47697 SDF-1(1-17) - (G)4
19	163.5	93.4	34	23	AAB47699 SDF-1(1-17) - (G)4
20	158.5	90.6	30	23	AAB47692 SDF-1(1-14) - (G)3
21	158.5	90.6	30	23	AAB47694 SDF-1(1-14) - (G)3
22	156	89.1	33	23	AAB47696 SDF-1(1-17) - (G)3
23	156	89.1	33	23	AAB47698 SDF-1(1-17) - (G)3
24	155	88.6	27	21	AAB28544 Chemokine-derived
25	154.5	88.3	34	23	AAM48699 CXCR4 cyclic pepti
26	137	78.3	31	23	AAM48674 CXCR4 peptide anta
27	134	76.6	33	23	AAB47710 SDF-1(1-14) - (G)4
28	132	75.4	25	21	AAB28546 Chemokine-derived
29	132	75.4	31	23	AAM48680 CXCR4 peptide anta
30	130	74.3	31	23	AAM48679 CXCR4 peptide anta
31	130	74.3	31	23	AAM48682 CXCR4 peptide anta
32	129.5	74.0	28	23	AAM48673 CXCR4 peptide anta
33	127	72.6	31	23	AAM48681 CXCR4 peptide anta
34	124.5	71.1	28	23	AAM48676 CXCR4 peptide anta
35	123	70.3	27	21	AAB28547 Chemokine-derived
36	123	70.3	29	23	AAM48694 CXCR4 peptide anta
37	122.5	70.0	28	23	AAM48675 CXCR4 peptide anta
38	122.5	70.0	28	23	AAM48678 CXCR4 peptide anta
39	122.5	70.0	30	23	AAM48687 CXCR4 peptide anta
40	122.5	70.0	30	23	AAM48688 CXCR4 peptide anta
41	121.5	69.4	30	23	AAM48690 CXCR4 peptide anta
42	119.5	68.3	28	23	AAM48677 CXCR4 peptide anta
43	119.5	68.3	30	23	AAM48689 CXCR4 peptide anta
44	117	66.9	67	19	AAM50760 Peptide which bind
45	117	66.9	67	20	AAV34092 Native stromal cel

ALIGNMENTS

RESULT 1	
AAB47686	standard; peptide: 31 AA.
XX	
AC	AAB47686;
XX	
DT	30-JAN-2002 (first entry)
XX	
DE	SDF-1(1-14) - (G)4 - SDF-1(56-67).
XX	
KW	Haematopoietic cell; multiplication; CXCR4 chemokine receptor 4; CXCR4; agonist; stromal cell derived factor one; SDF-1; autoimmune disease; macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer; autologous; allogenic; bone marrow; stem cell; transplantation.
XX	
OS	Synthetic.
XX	
PN	WO200176615-A2.
XX	
PD	18-OCT-2001.
XX	
PF	12-APR-2001; 2001WO-CA00540.
XX	
PR	12-APR-2000; 2000CA-2305036.
PR	14-SEP-2000; 2000US-232425P.
PR	23-FEB-2001; 2001CA-2335109.
XX	
PA	(UYBR-) UNIV BRITISH COLUMBIA.
PA	(CHEM-) CHEMOKINE THERAPEUTICS CORP.
XX	
PI	Salari H, Merzouk A, Arab L, Tudan CR, Saxena G, Eaves CJ; Cashman J, Clark-Lewis I;

XX WPI; 2002-025882/03.
DR CXC receptor 4 agonists that reduces hematopoietic cell multiplication
XX and susceptibility to cytotoxic agents, are useful for bone marrow or
PT peripheral blood stem cell transplantation
XX
XX Claim 8; Page 58; 74pp; English.
PS
CC The sequences given in AAB47680-717 represent peptides which may be
CC used in the method of the invention for reducing the rate of
CC hematopoietic cell multiplication. These peptides act as CXC chemokine
CC receptor 4 (CXCR4) agonists to the cells. These peptides are based on
CC stromal cell derived factor one (SDF-1) with some also containing
CC sequences derived from macrophage inflammatory protein 1-alpha
CC (MIP-1-alpha). They can be used to reduce susceptibility of
CC hematopoietic cells to a cytotoxic agent, by administering one of the
CC agonist peptides to the cells prior to or during exposure of the
CC cells to the cytotoxic agent. The CXCR4 agonist is used to reduce
CC susceptibility of hematopoietic cells to a cytotoxic agent, particularly
CC in a patient with cancer requiring autologous or allogenic bone marrow
CC or peripheral blood stem cell transplantation, or an autoimmune disease.
CC
XX Sequence 31 AA;
SQ

Query Match 100.0%; Score 175; DB 23; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.9e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVSLSYRCPCRFFGGGLKWIQYLEKALN 31
DB 1 KPVSLSYRCPCRFFGGGLKWIQYLEKALN 31

RESULT 2
AAB47693
ID AAB47693 standard; peptide; 31 AA.
XX
AC AAB47693;
XX
DT 30-JAN-2002 (first entry)
XX
DE SDF-1(1-14) - (G)4 - SDF-1(55-67) acid.
XX
KW Haematopoietic cell; multiplication; CXC chemokine receptor 4; CXCR4;
KW agonist; stromal cell derived factor one; SDF-1; autoimmune disease;
KW macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer;
KW autologous; allogenic; bone marrow; stem cell; transplantation.
XX
OS Synthetic.
XX
PN WO200176615-A2.
XX
PD 18-OCT-2001.
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PF 12-APR-2001; 2001WO-CA00540.
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PR 12-APR-2000; 2000CA-2305036.
PR 14-SEP-2000; 2000US-232425P.
PR 23-FEB-2001; 2001CA-2335109.
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PI Salari H, Merzouk A, Arab L, Tudan CR, Saxena G, Eaves CJ;
PI Cashman J, Clark-Lewis I;
XX
DR WPI; 2002-025882/03.
XX
PT CXC receptor 4 agonists that reduces hematopoietic cell multiplication
PT and susceptibility to cytotoxic agents, are useful for bone marrow or
PT peripheral blood stem cell transplantation
XX

PS Example 1; Page 42; 74pp; English.
XX
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CC used in the method of the invention for reducing the rate of
CC hematopoietic cell multiplication. These peptides act as CXC chemokine
CC receptor 4 (CXCR4) agonists to the cells. These peptides are based on
CC stromal cell derived factor one (SDF-1) with some also containing
CC sequences derived from macrophage inflammatory protein 1-alpha
CC (MIP-1-alpha). They can be used to reduce susceptibility of
CC hematopoietic cells to a cytotoxic agent, by administering one of the
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CC cells to the cytotoxic agent. The CXCR4 agonist is used to reduce
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CC in a patient with cancer requiring autologous or allogenic bone marrow
CC or peripheral blood stem cell transplantation, or an autoimmune disease.
CC
XX Sequence 31 AA;
SQ

Query Match 100.0%; Score 175; DB 23; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.9e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVSLSYRCPCRFFGGGLKWIQYLEKALN 31
DB 1 KPVSLSYRCPCRFFGGGLKWIQYLEKALN 31

RESULT 3
AAB47695
ID AAB47695 standard; peptide; 31 AA.
XX
AC AAB47695;
XX
DT 30-JAN-2002 (first entry)
XX
DE SDF-1(1-14) - (G)4 - SDF-1(55-67) amide.
XX
KW Haematopoietic cell; multiplication; CXC chemokine receptor 4; CXCR4;
KW agonist; stromal cell derived factor one; SDF-1; autoimmune disease;
KW macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer;
KW autologous; allogenic; bone marrow; stem cell; transplantation.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FH Modified-site 31
FT /note= "C-terminal amide"
XX
PN WO200176615-A2.
XX
PD 18-OCT-2001.
XX
PF 12-APR-2001; 2001WO-CA00540.
XX
PR 12-APR-2000; 2000CA-2305036.
PR 14-SEP-2000; 2000US-232425P.
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DR WPI; 2002-025882/03.
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CC susceptibility of hematopoietic cells to a cytotoxic agent, particularly
CC in a patient with cancer requiring autologous or allogenic bone marrow
CC or peripheral blood stem cell transplantation, or an autoimmune disease.
XX
SQ Sequence 31 AA;

Query Match 100.0%; Score 175; DB 23; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.9e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVSLSYRCPRCRFFGGGGLKWIQIYLEKALN 31
1 KPVSLSYRCPRCRFFGGGGLKWIQIYLEKALN 31
Db

RESULT 4
AAB47700
ID AAB47700 standard; peptide; 31 AA.
XX
AC AAB47700;
XX
DT 30-JAN-2002 (first entry)
XX
DE SDF-1(1-14) - (G)4 - SDF-1(55-67)-E24/K28-cyclic acid.
XX
KW Haematopoietic cell; multiplication; CXCR4 chemokine receptor 4; CXCR4;
KW agonist; stromal cell derived factor one; SDF-1; autoimmune disease;
KW macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer;
KW autologous; allogenic; bone marrow; stem cell; transplantation.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 24..28
FT /note= "Joined by side chain cyclization using
FT lactam formation"
XX
XX
PN WO200176615-A2.
XX
PD 18-OCT-2001.
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PF 12-APR-2001; 2001WO-CA00540.
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PR 12-APR-2000; 2000CA-2305036.
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DR WPI; 2002-025882/03.
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CC in a patient with cancer requiring autologous or allogenic bone marrow
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XX
SQ Sequence 31 AA;

Query Match 100.0%; Score 175; DB 23; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.9e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 KPVSLSYRCPRCRFFGGGGLKWIQIYLEKALN 31
Db

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AC AAB47701;
XX
DT 30-JAN-2002 (first entry)
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DE SDF-1(1-14) - (G)4 - SDF-1(55-67)-K20/E24-cyclic acid.
XX
KW Haematopoietic cell; multiplication; CXCR4 chemokine receptor 4; CXCR4;
KW agonist; stromal cell derived factor one; SDF-1; autoimmune disease;
KW macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer;
KW autologous; allogenic; bone marrow; stem cell; transplantation.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 20..24
FT /note= "Joined by side chain cyclization using
FT lactam formation"
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PN WO200176615-A2.
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PD 18-OCT-2001.
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PF 12-APR-2001; 2001WO-CA00540.
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DR WPI; 2002-025882/03.
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 XX
 SQ Sequence 31 AA;

Query Match 100.0%; Score 175; DB 23; Length 31;
 Best Local Similarity 100.0%; Pred. No. 1.9e-17;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVSLSYRCPCRRFFGGGLKWIQYLEKALN 31
 Db 1 KPVSLSYRCPCRRFFGGGLKWIQYLEKALN 31

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AAB47702
 ID AAB47702 standard; peptide; 31 AA.

XX
 AC AAB47702;

DT 30-JAN-2002 (first entry)

DE SDF-1(1-14) - (G)4 - SDF-1(55-67)-E24/K28-cyclic amide.

XX
 KW Haematopoietic cell; multiplication; CXC chemokine receptor 4; CXCR4;
 KW agonist; stromal cell derived factor one; SDF-1; autoimmune disease;
 KW macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer;
 KW autologous; allogenic; bone marrow; stem cell; transplantation.
 XX
 OS Synthetic.

XX
 FH Key Location/Qualifiers

FT Modified-site 24.28
 FT /note= "Joined by side chain cyclization using
 FT lactam formation"

FT Modified-site 31
 FT /note= "C-terminal amide"

XX
 PN WO200176615-A2.

PD 18-OCT-2001.

PF 12-APR-2001; 2001WO-CA00540.

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 SQ Sequence 31 AA;

Query Match 100.0%; Score 175; DB 23; Length 31;
 Best Local Similarity 100.0%; Pred. No. 1.9e-17;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVSLSYRCPCRRFFGGGLKWIQYLEKALN 31
 Db 1 KPVSLSYRCPCRRFFGGGLKWIQYLEKALN 31

RESULT 7

AAB47703
 ID AAB47703 standard; peptide; 31 AA.

XX
 AC AAB47703;

DT 30-JAN-2002 (first entry)

DE SDF-1(1-14) - (G)4 - SDF-1(55-67)-K20/E24-cyclic amide.

XX
 KW Haematopoietic cell; multiplication; CXC chemokine receptor 4; CXCR4;
 KW agonist; stromal cell derived factor one; SDF-1; autoimmune disease;
 KW macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer;
 KW autologous; allogenic; bone marrow; stem cell; transplantation.
 XX
 OS Synthetic.

XX
 FH Key Location/Qualifiers

FT Modified-site 20.24
 FT /note= "Joined by side chain cyclization using
 FT lactam formation"

FT Modified-site 31
 FT /note= "C-terminal amide"

XX
 PN WO200176615-A2.

PD 18-OCT-2001.

PF 12-APR-2001; 2001WO-CA00540.

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 PR 12-APR-2000; 2000CA-2305036.

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Query Match 100.0%; Score 175; DB 23; Length 31;
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Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVSLSYRCPCRFFGGGGLKWIQELYLEKALN 31
   |||||
Db 1 KPVSLSYRCPCRFFGGGGLKWIQELYLEKALN 31

RESULT 8
AAB47706
ID AAB47706 standard; peptide; 31 AA.
XX
AC AAB47706;
XX
DT 30-JAN-2002 (first entry)
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DE SDF-1(1-14) - (G)4 - SDF-1(55-67)-C9/C11-cyclic acid.
XX
KW Haematopoietic cell; multiplication; CXC chemokine receptor 4; CXCR4;
KW agonist; stromal cell derived factor one; SDF-1; autoimmune disease;
KW macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer;
KW autologous; allogenic; bone marrow; stem cell; transplantation.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Disulfide-bond 9..11
XX
PN WO200176615-A2.
PD 18-OCT-2001.
XX
PF 12-APR-2001; 2001WO-CA00540.
XX
PR 12-APR-2000; 2000CA-2305036.
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PI Salari H, Merzouk A, Arab L, Tudan CR, Saxena G, Eaves CJ;
PI Cashman J, Clark-Lewis I;
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DR WPI; 2002-025882/03.
XX
PT CXC receptor 4 agonists that reduces hematopoietic cell multiplication
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CC hematopoietic cell multiplication. These peptides act as CXC chemokine
CC receptor 4 (CXCR4) agonists to the cells. These peptides are based on
CC stromal cell derived factor one (SDF-1) with some also containing
CC sequences derived from macrophage inflammatory protein 1-alpha
CC (MIP-1-alpha). They can be used to reduce susceptibility of
CC hematopoietic cells to a cytotoxic agent, by administering one of the
CC agonist peptides to the cells prior to or during exposure of the
```

```
CC cells to the cytotoxic agent. The CXCR4 agonist is used to reduce
CC susceptibility of hematopoietic cells to a cytotoxic agent, particularly
CC in a patient with cancer requiring autologous or allogenic bone marrow
CC or peripheral blood stem cell transplantation, or an autoimmune disease.
XX
SQ Sequence 31 AA;

Query Match 100.0%; Score 175; DB 23; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.9e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVSLSYRCPCRFFGGGGLKWIQELYLEKALN 31
   |||||
Db 1 KPVSLSYRCPCRFFGGGGLKWIQELYLEKALN 31

RESULT 9
AAB47707
ID AAB47707 standard; peptide; 31 AA.
XX
AC AAB47707;
XX
DT 30-JAN-2002 (first entry)
XX
DE SDF-1(1-14) - (G)4 - SDF-1(55-67)-C9/C11-cyclic amide.
XX
KW Haematopoietic cell; multiplication; CXC chemokine receptor 4; CXCR4;
KW agonist; stromal cell derived factor one; SDF-1; autoimmune disease;
KW macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer;
KW autologous; allogenic; bone marrow; stem cell; transplantation.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Disulfide-bond 9..11
FT Modified-site 31
FT /note= "C-terminal amide"
XX
PN WO200176615-A2.
PD 18-OCT-2001.
XX
PF 12-APR-2001; 2001WO-CA00540.
XX
PR 12-APR-2000; 2000CA-2305036.
PR 14-SEP-2000; 2000US-232425P.
PR 23-FEB-2001; 2001CA-2335109.
XX
PA (UYBR-) UNIV BRITISH COLUMBIA.
PA (CHEM-) CHEMOKINE THERAPEUTICS CORP.
XX
PI Salari H, Merzouk A, Arab L, Tudan CR, Saxena G, Eaves CJ;
PI Cashman J, Clark-Lewis I;
XX
DR WPI; 2002-025882/03.
XX
PT CXC receptor 4 agonists that reduces hematopoietic cell multiplication
PT and susceptibility to cytotoxic agents, are useful for bone marrow or
PT peripheral blood stem cell transplantation
XX
PS Example 1; Page 44; 74pp; English.
XX
CC The sequences given in AAB47680-717 represent peptides which may be
CC used in the method of the invention for reducing the rate of
CC hematopoietic cell multiplication. These peptides act as CXC chemokine
CC receptor 4 (CXCR4) agonists to the cells. These peptides are based on
CC stromal cell derived factor one (SDF-1) with some also containing
CC sequences derived from macrophage inflammatory protein 1-alpha
CC (MIP-1-alpha). They can be used to reduce susceptibility of
CC hematopoietic cells to a cytotoxic agent, by administering one of the
CC agonist peptides to the cells prior to or during exposure of the
CC cells to the cytotoxic agent. The CXCR4 agonist is used to reduce
CC susceptibility of hematopoietic cells to a cytotoxic agent, particularly
```

CC in a patient with cancer requiring autologous or allogenic bone marrow
 CC or peripheral blood stem cell transplantation, or an autoimmune disease.
 XX
 SQ Sequence 31 AA;

Query Match 100.0%; Score 175; DB 23; Length 31;
 Best Local Similarity 100.0%; Pred. No. 1.9e-17;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KPVSLSYRCPCRFFGGGGLKWIQYLEKALN 31
 DB 1 KPVSLSYRCPCRFFGGGGLKWIQYLEKALN 31

RESULT 10
 AAB47714
 ID AAB47714 standard; peptide; 31 AA.

AC AAB47714;
 DT 30-JAN-2002 (first entry)
 DE SDF-1(1-14) - (G)4 - SDF-1(55-67) acid.
 KW Haematopoietic cell; multiplication; CXC chemokine receptor 4; CXCR4;
 KW agonist; stromal cell derived factor one; SDF-1; autoimmune disease;
 KW macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer;
 KW autologous; allogenic; bone marrow; stem cell; transplantation.
 OS Synthetic.
 WO200176615-A2.

18-OCT-2001.
 12-APR-2001; 2001WO-CA00540.
 12-APR-2000; 2000CA-2305036.
 14-SEP-2000; 2000US-232425P.
 23-FEB-2001; 2001CA-2335109.

(UYBR-) UNIV BRITISH COLUMBIA.
 (CHEM-) CHEMOKINE THERAPEUTICS CORP.

PI Salari H, Merzouk A, Arab L, Tudan CR, Saxena G, Eaves CJ;
 PI Cashman J, Clark-Lewis I;
 DR WPI; 2002-025882/03.

CXC receptor 4 agonists that reduces hematopoietic cell multiplication
 and susceptibility to cytotoxic agents, are useful for bone marrow or
 peripheral blood stem cell transplantation

Example 1; Page 47; 74pp; English.

The sequences given in AAB47680-717 represent peptides which may be
 used in the method of the invention for reducing the rate of
 hematopoietic cell multiplication. These peptides act as CXC chemokine
 receptor 4 (CXCR4) agonists to the cells. These peptides are based on
 stromal cell derived factor one (SDF-1) with some also containing
 sequences derived from macrophage inflammatory protein 1-alpha
 (MIP-1-alpha). They can be used to reduce susceptibility of
 hematopoietic cells to a cytotoxic agent, by administering one of the
 agonist peptides to the cells prior to or during exposure of the
 cells to the cytotoxic agent. The CXCR4 agonist is used to reduce
 susceptibility of hematopoietic cells to a cytotoxic agent, particularly
 in a patient with cancer requiring autologous or allogenic bone marrow
 or peripheral blood stem cell transplantation, or an autoimmune disease.

Query Match 100.0%; Score 175; DB 23; Length 31;
 Best Local Similarity 100.0%; Pred. No. 1.9e-17;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 KPVSLSYRCPCRFFGGGGLKWIQYLEKALN 31
 DB 1 KPVSLSYRCPCRFFGGGGLKWIQYLEKALN 31

RESULT 11
 AAB47715
 ID AAB47715 standard; peptide; 31 AA.

AC AAB47715;
 DT 30-JAN-2002 (first entry)
 DE SDF-1(1-14) - (G)4 - SDF-1(55-67) amide.
 KW Haematopoietic cell; multiplication; CXC chemokine receptor 4; CXCR4;
 KW agonist; stromal cell derived factor one; SDF-1; autoimmune disease;
 KW macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer;
 KW autologous; allogenic; bone marrow; stem cell; transplantation.
 OS Synthetic.

Key Location/Qualifiers
 Modified-site 31
 /note= "C-terminal amide"

WO200176615-A2.
 18-OCT-2001.
 12-APR-2001; 2001WO-CA00540.
 12-APR-2000; 2000CA-2305036.
 14-SEP-2000; 2000US-232425P.
 23-FEB-2001; 2001CA-2335109.

(UYBR-) UNIV BRITISH COLUMBIA.
 (CHEM-) CHEMOKINE THERAPEUTICS CORP.

PI Salari H, Merzouk A, Arab L, Tudan CR, Saxena G, Eaves CJ;
 PI Cashman J, Clark-Lewis I;
 DR WPI; 2002-025882/03.

CXC receptor 4 agonists that reduces hematopoietic cell multiplication
 and susceptibility to cytotoxic agents, are useful for bone marrow or
 peripheral blood stem cell transplantation

Example 1; Page 47; 74pp; English.

The sequences given in AAB47680-717 represent peptides which may be
 used in the method of the invention for reducing the rate of
 hematopoietic cell multiplication. These peptides act as CXC chemokine
 receptor 4 (CXCR4) agonists to the cells. These peptides are based on
 stromal cell derived factor one (SDF-1) with some also containing
 sequences derived from macrophage inflammatory protein 1-alpha
 (MIP-1-alpha). They can be used to reduce susceptibility of
 hematopoietic cells to a cytotoxic agent, by administering one of the
 agonist peptides to the cells prior to or during exposure of the
 cells to the cytotoxic agent. The CXCR4 agonist is used to reduce
 susceptibility of hematopoietic cells to a cytotoxic agent, particularly
 in a patient with cancer requiring autologous or allogenic bone marrow
 or peripheral blood stem cell transplantation, or an autoimmune disease.

Query Match 100.0%; Score 175; DB 23; Length 31;
 Best Local Similarity 100.0%; Pred. No. 1.9e-17;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KPVSLSYRCPCRFFGGGGLKWIQYLEKALN 31

Db 1 KPVSLSYRCPCRFEGGGGLKWIQIYLEKALN 31

RESULT 12
AAB47716
ID AAB47716 standard; peptide; 31 AA.
XX
AC AAB47716;
XX
DT 30-JAN-2002 (first entry)
XX
DE SDF-1(1-14) - (G)4 - SDF-1(55-67)-E24/K28-cyclic amide.
XX
KW Haematopoietic cell; multiplication; CXC chemokine receptor 4; CXCR4;
KW agonist; stromal cell derived factor one; SDF-1; autoimmune disease;
KW macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer;
KW autologous; allogenic; bone marrow; stem cell; transplantation.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 24..28
FT /note= "Joined by side chain cyclization using
FT lactam formation"
FT Modified-site 31
FT /note= "C-terminal amide"
XX
PN WO200176615-A2.
XX
PD 18-OCT-2001.
XX
PF 12-APR-2001; 2001WO-CA00540.
XX
PR 12-APR-2000; 2000CA-2305036.
PR 14-SEP-2000; 2000US-232425P.
PR 23-FEB-2001; 2001CA-2335109.
XX
PA (UYBR-) UNIV BRITISH COLUMBIA.
PA (CHEM-) CHEMOKINE THERAPEUTICS CORP.
XX
PI Salari H, Merzouk A, Arab L, Tudan CR, Saxena G, Eaves CJ;
PI Cashman J, Clark-Lewis I;
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DR WPI; 2002-025882/03.
XX
PT CXC receptor 4 agonists that reduces hematopoietic cell multiplication
PT and susceptibility to cytotoxic agents, are useful for bone marrow or
PT peripheral blood stem cell transplantation
XX
PS Example 1; Page 47; 74pp; English.
XX
CC The sequences given in AAB47680-717 represent peptides which may be
CC used in the method of the invention for reducing the rate of
CC hematopoietic cell multiplication. These peptides act as CXC chemokine
CC receptor 4 (CXCR4) agonists to the cells. These peptides are based on
CC stromal cell derived factor one (SDF-1) with some also containing
CC sequences derived from macrophage inflammatory protein 1-alpha
CC (MIP-1-alpha). They can be used to reduce susceptibility of
CC hematopoietic cells to a cytotoxic agent, by administering one of the
CC agonist peptides to the cells prior to or during exposure of the
CC cells to the cytotoxic agent. The CXCR4 agonist is used to reduce
CC susceptibility of hematopoietic cells to a cytotoxic agent, particularly
CC in a patient with cancer requiring autologous or allogenic bone marrow
CC or peripheral blood stem cell transplantation, or an autoimmune disease.
XX
SQ Sequence 31 AA;

Query Match 100.0%; Score 175; DB 23; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.9e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KPVSLSYRCPCRFEGGGGLKWIQIYLEKALN 31

Db 1 KPVSLSYRCPCRFEGGGGLKWIQIYLEKALN 31

RESULT 13
AAB47717
ID AAB47717 standard; peptide; 31 AA.
XX
AC AAB47717;
XX
DT 30-JAN-2002 (first entry)
XX
DE SDF-1(1-14) - (G)4 - SDF-1(55-67)-K20/E24-cyclic amide.
XX
KW Haematopoietic cell; multiplication; CXC chemokine receptor 4; CXCR4;
KW agonist; stromal cell derived factor one; SDF-1; autoimmune disease;
KW macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer;
KW autologous; allogenic; bone marrow; stem cell; transplantation.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 20..24
FT /note= "Joined by side chain cyclization using
FT lactam formation"
FT Modified-site 31
FT /note= "C-terminal amide"
XX
PN WO200176615-A2.
XX
PD 18-OCT-2001.
XX
PF 12-APR-2001; 2001WO-CA00540.
XX
PR 12-APR-2000; 2000CA-2305036.
PR 14-SEP-2000; 2000US-232425P.
PR 23-FEB-2001; 2001CA-2335109.
XX
PA (UYBR-) UNIV BRITISH COLUMBIA.
PA (CHEM-) CHEMOKINE THERAPEUTICS CORP.
XX
PI Salari H, Merzouk A, Arab L, Tudan CR, Saxena G, Eaves CJ;
PI Cashman J, Clark-Lewis I;
XX
DR WPI; 2002-025882/03.
XX
PT CXC receptor 4 agonists that reduces hematopoietic cell multiplication
PT and susceptibility to cytotoxic agents, are useful for bone marrow or
PT peripheral blood stem cell transplantation
XX
PS Example 1; Page 47; 74pp; English.
XX
CC The sequences given in AAB47680-717 represent peptides which may be
CC used in the method of the invention for reducing the rate of
CC hematopoietic cell multiplication. These peptides act as CXC chemokine
CC receptor 4 (CXCR4) agonists to the cells. These peptides are based on
CC stromal cell derived factor one (SDF-1) with some also containing
CC sequences derived from macrophage inflammatory protein 1-alpha
CC (MIP-1-alpha). They can be used to reduce susceptibility of
CC hematopoietic cells to a cytotoxic agent, by administering one of the
CC agonist peptides to the cells prior to or during exposure of the
CC cells to the cytotoxic agent. The CXCR4 agonist is used to reduce
CC susceptibility of hematopoietic cells to a cytotoxic agent, particularly
CC in a patient with cancer requiring autologous or allogenic bone marrow
CC or peripheral blood stem cell transplantation, or an autoimmune disease.
XX
SQ Sequence 31 AA;

Query Match 100.0%; Score 175; DB 23; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.9e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KPVSLSYRCPCRFEGGGGLKWIQIYLEKALN 31

Db 1 KPVSLSYRCPCRFFGGGLKWIQYLYLEKALN 31

RESULT 14

AAB47704 AAB47704 standard; peptide; 31 AA.

AC AAB47704;

DT 30-JAN-2002 (first entry)

DE SDF-1(1-14) - (G)4 - SDF-1(55-67)-K20/D24-cyclic acid.

KW Haematopoietic cell; multiplication; CXC chemokine receptor 4; CXCR4; agonist; stromal cell derived factor one; SDF-1; autoimmune disease; macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer; autologous; allogenic; bone marrow; stem cell; transplantation.

OS Synthetic.

FH Key Location/Qualifiers
FT Modified-site 20..24
FT /note= "Joined by side chain cyclization using lactam formation"

FT Misc-difference 24
FT /label= E24D

FT Modified-site 24..28
FT /note= "Can be joined by side chain cyclization using lactam formation"

PN WO200176615-A2.

PD 18-OCT-2001.

PF 12-APR-2001; 2001WO-CA00540.

PR 12-APR-2000; 2000CA-2305036.

PR 14-SEP-2000; 2000US-232425P.

PR 23-FEB-2001; 2001CA-2335109.

PA (UYBR-) UNIV BRITISH COLUMBIA.

PA (CHEM-) CHEMOKINE THERAPEUTICS CORP.

PI Salari H, Merzouk A, Arab L, Tudan CR, Saxena G, Eaves CJ;

PI Cashman J, Clark-Lewis I;

DR WPI; 2002-025882/03.

PT CXC receptor 4 agonists that reduces hematopoietic cell multiplication and susceptibility to cytotoxic agents, are useful for bone marrow or peripheral blood stem cell transplantation

PS Example 1; Page 44; 74pp; English.

CC The sequences given in AAB47680-717 represent peptides which may be used in the method of the invention for reducing the rate of hematopoietic cell multiplication. These peptides act as CXC chemokine receptor 4 (CXCR4) agonists to the cells. These peptides are based on stromal cell derived factor one (SDF-1) with some also containing sequences derived from macrophage inflammatory protein 1-alpha (MIP-1-alpha). They can be used to reduce susceptibility of hematopoietic cells to a cytotoxic agent, by administering one of the agonist peptides to the cells prior to or during exposure of the cells to the cytotoxic agent. The CXCR4 agonist is used to reduce susceptibility of hematopoietic cells to a cytotoxic agent, particularly in a patient with cancer requiring autologous or allogenic bone marrow or peripheral blood stem cell transplantation, or an autoimmune disease.

Sequence 31 AA;

Query Match 98.3%; Score 172; DB 23; Length 31;
Best Local Similarity 96.8%; Pred. No. 5.1e-17;

Matches 30; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
CY 1 KPVSLSYRCPCRFFGGGLKWIQYLYLEKALN 31
Db 1 KPVSLSYRCPCRFFGGGLKWIQYLYLEKALN 31

RESULT 15

AAB47705 AAB47705 standard; peptide; 31 AA.

AC AAB47705;

DT 30-JAN-2002 (first entry)

DE SDF-1(1-14) - (G)4 - SDF-1(55-67)-K20/D24-cyclic amide.

KW Haematopoietic cell; multiplication; CXC chemokine receptor 4; CXCR4; agonist; stromal cell derived factor one; SDF-1; autoimmune disease; macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer; autologous; allogenic; bone marrow; stem cell; transplantation.

OS Synthetic.

FH Key Location/Qualifiers
FT Modified-site 20..24
FT /note= "Joined by side chain cyclization using lactam formation"

FT Misc-difference 24
FT /label= E24D

FT Modified-site 24..28
FT /note= "Can be joined by side chain cyclization using lactam formation"

FT Modified-site 31
FT /note= "C-terminal amide"

PN WO200176615-A2.

PD 18-OCT-2001.

PF 12-APR-2001; 2001WO-CA00540.

PR 12-APR-2000; 2000CA-2305036.

PR 14-SEP-2000; 2000US-232425P.

PR 23-FEB-2001; 2001CA-2335109.

PA (UYBR-) UNIV BRITISH COLUMBIA.

PA (CHEM-) CHEMOKINE THERAPEUTICS CORP.

PI Salari H, Merzouk A, Arab L, Tudan CR, Saxena G, Eaves CJ;

PI Cashman J, Clark-Lewis I;

DR WPI; 2002-025882/03.

PT CXC receptor 4 agonists that reduces hematopoietic cell multiplication and susceptibility to cytotoxic agents, are useful for bone marrow or peripheral blood stem cell transplantation

PS Example 1; Page 44; 74pp; English.

CC The sequences given in AAB47680-717 represent peptides which may be used in the method of the invention for reducing the rate of hematopoietic cell multiplication. These peptides act as CXC chemokine receptor 4 (CXCR4) agonists to the cells. These peptides are based on stromal cell derived factor one (SDF-1) with some also containing sequences derived from macrophage inflammatory protein 1-alpha (MIP-1-alpha). They can be used to reduce susceptibility of hematopoietic cells to a cytotoxic agent, by administering one of the agonist peptides to the cells prior to or during exposure of the cells to the cytotoxic agent. The CXCR4 agonist is used to reduce susceptibility of hematopoietic cells to a cytotoxic agent, particularly in a patient with cancer requiring autologous or allogenic bone marrow or peripheral blood stem cell transplantation, or an autoimmune disease.

Db 1 KPVSLSYRCPORFFGGGLKWIQIYLEKALN 31

RESULT 12
AAB47716

ID AAB47716 standard; peptide; 31 AA.

XX AAB47716;

DT 30-JAN-2002 (first entry)

DE SDF-1(1-14) - (G)4 - SDF-1(55-67)-E24/K28-cyclic amide.

XX Haematopoietic cell; multiplication; CXC chemokine receptor 4; CXCR4;
KW agonist; stromal cell derived factor one; SDF-1; autoimmune disease;
KW macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer;
KW autologous; allogenic; bone marrow; stem cell; transplantation.

XX Synthetic.

OS Key Location/Qualifiers

FT Modified-site 24..28

FT /note= "Joined by side chain cyclization using lactam formation"

FT Modified-site 31 /note= "C-terminal amide"

XX WO200176615-A2.

XX 18-OCT-2001.

XX 12-APR-2001; 2001WO-CA00540.

XX 12-APR-2000; 2000CA-2305036.

XX 14-SEP-2000; 2000US-232425P.

XX 23-FEB-2001; 2001CA-2335109.

XX (UYBR-) UNIV BRITISH COLUMBIA.

XX (CHEM-) CHEMOKINE THERAPEUTICS CORP.

XX Salari H, Merzouk A, Arab L, Tudan CR, Saxena G, Eaves CJ;

XX Cashman J, Clark-Lewis I;

XX WPI; 2002-025882/03.

XX CXC receptor 4 agonists that reduces hematopoietic cell multiplication

XX and susceptibility to cytotoxic agents, are useful for bone marrow or

XX peripheral blood stem cell transplantation

XX Example 1; Page 47; 74pp; English.

XX The sequences given in AAB47680-717 represent peptides which may be
CC used in the method of the invention for reducing the rate of
CC hematopoietic cell multiplication. These peptides act as CXC chemokine
CC receptor 4 (CXCR4) agonists to the cells. These peptides are based on
CC stromal cell derived factor one (SDF-1) with some also containing
CC sequences derived from macrophage inflammatory protein 1-alpha
CC (MIP-1-alpha). They can be used to reduce susceptibility of
CC hematopoietic cells to a cytotoxic agent, by administering one of the
CC agonist peptides to the cells prior to or during exposure of the
CC cells to the cytotoxic agent. The CXCR4 agonist is used to reduce
CC susceptibility of hematopoietic cells to a cytotoxic agent, particularly
CC in a patient with cancer requiring autologous or allogenic bone marrow
CC or peripheral blood stem cell transplantation, or an autoimmune disease.

XX Sequence 31 AA;

XX Query Match 100.0%; Score 175; DB 23; Length 31;

XX Best Local Similarity 100.0%; Pred. No. 1.9e-17;

XX Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KPVSLSYRCPORFFGGGLKWIQIYLEKALN 31

Db 1 KPVSLSYRCPORFFGGGLKWIQIYLEKALN 31

RESULT 13
AAB47717

ID AAB47717 standard; peptide; 31 AA.

XX AAB47717;

DT 30-JAN-2002 (first entry)

DE SDF-1(1-14) - (G)4 - SDF-1(55-67)-K20/E24-cyclic amide.

XX Haematopoietic cell; multiplication; CXC chemokine receptor 4; CXCR4;
KW agonist; stromal cell derived factor one; SDF-1; autoimmune disease;
KW macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer;
KW autologous; allogenic; bone marrow; stem cell; transplantation.

XX Synthetic.

OS Key Location/Qualifiers

FT Modified-site 20..24

FT /note= "Joined by side chain cyclization using lactam formation"

FT Modified-site 31 /note= "C-terminal amide"

XX WO200176615-A2.

XX 18-OCT-2001.

XX 12-APR-2001; 2001WO-CA00540.

XX 12-APR-2000; 2000CA-2305036.

XX 14-SEP-2000; 2000US-232425P.

XX 23-FEB-2001; 2001CA-2335109.

XX (UYBR-) UNIV BRITISH COLUMBIA.

XX (CHEM-) CHEMOKINE THERAPEUTICS CORP.

XX Salari H, Merzouk A, Arab L, Tudan CR, Saxena G, Eaves CJ;

XX Cashman J, Clark-Lewis I;

XX WPI; 2002-025882/03.

XX CXC receptor 4 agonists that reduces hematopoietic cell multiplication

XX and susceptibility to cytotoxic agents, are useful for bone marrow or

XX peripheral blood stem cell transplantation

XX Example 1; Page 47; 74pp; English.

XX The sequences given in AAB47680-717 represent peptides which may be
CC used in the method of the invention for reducing the rate of
CC hematopoietic cell multiplication. These peptides act as CXC chemokine
CC receptor 4 (CXCR4) agonists to the cells. These peptides are based on
CC stromal cell derived factor one (SDF-1) with some also containing
CC sequences derived from macrophage inflammatory protein 1-alpha
CC (MIP-1-alpha). They can be used to reduce susceptibility of
CC hematopoietic cells to a cytotoxic agent, by administering one of the
CC agonist peptides to the cells prior to or during exposure of the
CC cells to the cytotoxic agent. The CXCR4 agonist is used to reduce
CC susceptibility of hematopoietic cells to a cytotoxic agent, particularly
CC in a patient with cancer requiring autologous or allogenic bone marrow
CC or peripheral blood stem cell transplantation, or an autoimmune disease.

XX Sequence 31 AA;

XX Query Match 100.0%; Score 175; DB 23; Length 31;

XX Best Local Similarity 100.0%; Pred. No. 1.9e-17;

XX Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KPVSLSYRCPORFFGGGLKWIQIYLEKALN 31

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Db          |||||
1 KPVSLSYRCPCRFFGGGGLKWIQDYLERALN 31

RESULT 14
AAB47704
ID AAB47704 standard; peptide; 31 AA.
XX
AC AAB47704;
XX
DT 30-JAN-2002 (first entry)
XX
DE SDF-1(1-14) - (G)4 - SDF-1(55-67)-K20/D24-cyclic acid.
XX
KW Haematopoietic cell; multiplication; CXC chemokine receptor 4; CXCR4;
KW agonist; stromal cell derived factor one; SDF-1; autoimmune disease;
KW macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer;
KW autologous; allogenic; bone marrow; stem cell; transplantation.
XX
OS Synthetic.
XX
FH Key
FH Modified-site 20..24 Location/Qualifiers
FT /note= "Joined by side chain cyclization using
FT lactam formation"
FT Misc-difference 24 /label= E24D
FT Modified-site 24..28
FT /note= "Can be joined by side chain cyclization using
FT lactam formation"
XX
PN WO200176615-A2.
XX
PD 18-OCT-2001.
XX
PF 12-APR-2001; 2001WO-CA00540.
XX
PR 12-APR-2000; 2000CA-2305036.
PR 14-SEP-2000; 2000US-232425P.
PR 23-FEB-2001; 2001CA-2335109.
XX
PA (UYBR-) UNIV BRITISH COLUMBIA.
PA (CHEM-) CHEMOKINE THERAPEUTICS CORP.
XX
PI Salari H, Merzouk A, Arab L, Tudan CR, Saxena G, Eaves CJ;
PI Cashman J, Clark-Lewis I;
XX
DR WPI; 2002-025882/03.
XX
PT CXC receptor 4 agonists that reduces hematopoietic cell multiplication
PT and susceptibility to cytotoxic agents, are useful for bone marrow or
PT peripheral blood stem cell transplantation
XX
PS Example 1; Page 44; 74pp; English.
XX
CC The sequences given in AAB47680-717 represent peptides which may be
CC used in the method of the invention for reducing the rate of
CC hematopoietic cell multiplication. These peptides act as CXC chemokine
CC receptor 4 (CXCR4) agonists to the cells. These peptides are based on
CC stromal cell derived factor one (SDF-1) with some also containing
CC sequences derived from macrophage inflammatory protein 1-alpha
CC (MIP-1-alpha). They can be used to reduce susceptibility of
CC hematopoietic cells to a cytotoxic agent, by administering one of the
CC agonist peptides to the cells prior to or during exposure of the
CC cells to the cytotoxic agent. The CXCR4 agonist is used to reduce
CC susceptibility of hematopoietic cells to a cytotoxic agent, particularly
CC in a patient with cancer requiring autologous or allogenic bone marrow
CC or peripheral blood stem cell transplantation, or an autoimmune disease.
XX
SQ Sequence 31 AA;
Query Match 98.3%; Score 172; DB 23; Length 31;
Best Local Similarity 96.8%; Pred. No. 5.1e-17;
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Matches 30; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY          1 KPVSLSYRCPCRFFGGGGLKWIQDYLERALN 31
Db          1 KPVSLSYRCPCRFFGGGGLKWIQDYLERALN 31

RESULT 15
AAB47705
ID AAB47705 standard; peptide; 31 AA.
XX
AC AAB47705;
XX
DT 30-JAN-2002 (first entry)
XX
DE SDF-1(1-14) - (G)4 - SDF-1(55-67)-K20/D24-cyclic amide.
XX
KW Haematopoietic cell; multiplication; CXC chemokine receptor 4; CXCR4;
KW agonist; stromal cell derived factor one; SDF-1; autoimmune disease;
KW macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer;
KW autologous; allogenic; bone marrow; stem cell; transplantation.
XX
OS Synthetic.
XX
FH Key
FH Modified-site 20..24 Location/Qualifiers
FT /note= "Joined by side chain cyclization using
FT lactam formation"
FT Misc-difference 24 /label= E24D
FT Modified-site 24..28
FT /note= "Can be joined by side chain cyclization using
FT lactam formation"
FT Modified-site 31 /note= "C-terminal amide"
XX
PN WO200176615-A2.
XX
PD 18-OCT-2001.
XX
PF 12-APR-2001; 2001WO-CA00540.
XX
PR 12-APR-2000; 2000CA-2305036.
PR 14-SEP-2000; 2000US-232425P.
PR 23-FEB-2001; 2001CA-2335109.
XX
PA (UYBR-) UNIV BRITISH COLUMBIA.
PA (CHEM-) CHEMOKINE THERAPEUTICS CORP.
XX
PI Salari H, Merzouk A, Arab L, Tudan CR, Saxena G, Eaves CJ;
PI Cashman J, Clark-Lewis I;
XX
DR WPI; 2002-025882/03.
XX
PT CXC receptor 4 agonists that reduces hematopoietic cell multiplication
PT and susceptibility to cytotoxic agents, are useful for bone marrow or
PT peripheral blood stem cell transplantation
XX
PS Example 1; Page 44; 74pp; English.
XX
CC The sequences given in AAB47680-717 represent peptides which may be
CC used in the method of the invention for reducing the rate of
CC hematopoietic cell multiplication. These peptides act as CXC chemokine
CC receptor 4 (CXCR4) agonists to the cells. These peptides are based on
CC stromal cell derived factor one (SDF-1) with some also containing
CC sequences derived from macrophage inflammatory protein 1-alpha
CC (MIP-1-alpha). They can be used to reduce susceptibility of
CC hematopoietic cells to a cytotoxic agent, by administering one of the
CC agonist peptides to the cells prior to or during exposure of the
CC cells to the cytotoxic agent. The CXCR4 agonist is used to reduce
CC susceptibility of hematopoietic cells to a cytotoxic agent, particularly
CC in a patient with cancer requiring autologous or allogenic bone marrow
CC or peripheral blood stem cell transplantation, or an autoimmune disease.
```

XX Sequence 31 AA;

Query Match 98.3%; Score 172; DB 23; Length 31;
Best Local Similarity 96.8%; Pred. No. 5.1e-17;
Matches 30; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KPVSLSYRCPCRFEGGGGLKWIQYLEKALN 31
Db 1 KPVSLSYRCPCRFEGGGGLKWIQYLEKALN 31

Search completed: October 9, 2003, 09:19:01
Job time : 43 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 9, 2003, 09:17:42 ; Search time 39 Seconds
(without alignments)
76.442 Million cell updates/sec

Title: US-09-835-107A-11
Perfect score: 175
Sequence: 1 KPVSLSYRCPCRFFGGGLKWIQYLEKALN 31

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	117	66.9	89	2	A53497	pre-B-cell growth-
2	117	66.9	89	2	I53416	interleukin-8 homo
3	117	66.9	93	2	G01540	cytokine SDF-1-bet
4	117	66.9	93	2	I81182	cytokine - mouse
5	61	34.9	1084	2	T08583	cellulose synthase
6	61	34.9	1088	2	H84604	probable cellulose
7	60.5	34.6	974	2	T10797	cellulose synthase
8	58	33.1	469	2	C83345	probable class III
9	58	33.1	1081	2	T52028	cellulose synthase
10	56	32.0	233	2	T35594	hypothetical prote
11	54	30.9	398	2	T52311	isopenicillin N ep
12	53	30.3	454	2	C64104	gamma-aminobutyrat
13	53	30.3	470	2	T46814	gamma-aminobutyrat
14	53	30.3	470	2	B95419	diaminobutyrate-py
15	50	28.6	202	2	AI3489	cytochrome c-552 l
16	50	28.6	588	2	S34786	catechol oxidase (
17	50	28.6	685	2	T10800	cellulose synthase
18	49.5	28.3	170	2	B85359	hypothetical prote
19	49.5	28.3	577	2	I50731	lg heavy chain - n
20	49	28.0	386	2	C81419	probable type IIS
21	49	28.0	508	2	F87198	glycerol kinase [i
22	49	28.0	517	2	A70793	probable glycerol
23	49	28.0	556	1	A53376	tryptophan 2-mono
24	49	28.0	557	1	A25493	tryptophan 2-mono
25	49	28.0	1722	2	A88470	protein C28H8.3 [i
26	48	27.4	189	2	D69389	DNA-directed RNA p
27	48	27.4	309	1	S34198	IgE Fc receptor II
28	48	27.4	331	1	LNMSER	IgE Fc receptor, I
29	48	27.4	383	2	C90136	26S proteasome SU

30	48	27.4	593	2	S30958	gene 13 protein -
31	48	27.4	661	2	S45131	probable membrane
32	48	27.4	1016	2	F82159	transporter, Acrb/
33	48	27.4	1429	2	S06434	homeotic protein 1
34	47.5	27.1	439	2	E72298	hypothetical prote
35	47.5	27.1	722	2	H96986	endo-1,4-beta gluc
36	47	26.9	203	2	I50481	synapse protein SN
37	47	26.9	398	2	S30901	isopenicillin N ep
38	47	26.9	409	2	S01825	transforming growt
39	47	26.9	623	2	T40685	phosphatidylcholin
40	47	26.9	1108	2	T35827	probable membrane
41	47	26.9	1400	2	T22644	hypothetical prote
42	46.5	26.6	1112	2	D96753	similar to disease
43	46.5	26.6	1287	2	T22235	hypothetical prote
44	46	26.3	122	2	T45165	succinate dehydrog
45	46	26.3	212	2	S73466	probable DNA prima

ALIGNMENTS

RESULT 1
A53497
pre-B-cell growth-stimulating factor precursor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 20-Jun-2000
C:Accession: A53497; I59582
R:Nagasawa, T.; Kikutani, H.; Kishimoto, T.
Proc. Natl. Acad. Sci. U.S.A. 91, 2305-2309, 1994
A:Title: Molecular cloning and structure of a pre-B-cell growth-stimulating factor.
A:Reference number: A53497; MUID:94181581; PMID:8134392
A:Accession: A53497.
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-89 <NAG>
A:Cross-references: GB:D21072; NID:9413905; PIDN:BA04648.1; PID:9468457
R:Tashiro, K.; Tada, H.; Heilker, R.; Shirozu, M.; Nakano, T.; Honjo, T.
Science 261, 600-603, 1993
A:Title: Signal sequence trap: a cloning strategy for secreted proteins and type I me
A:Reference number: I59582; MUID:93342488; PMID:8342023
A:Accession: I59582
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-89 <RES>
A:Cross-references: GB:L12029; NID:9393179; PIDN:AAA0100.1; PID:9393180
C:Genetics:
A:Gene: SDF-1-alpha
C:Superfamily: beta-thromboglobulin
C:Keywords: cytokine
Query Match 66.9%; Score 117; DB 2; Length 89;
Best local Similarity 40.3%; Pred. No. 4.8e-09;
Matches 27; Conservative 0; Mismatches 4; Indels 36; Gaps 1;
QY 1 KPVSLSYRCPCRFFGG-----GGLKWIQ 24
DB 22 KPVSLSYRCPCRFFESHIAANVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKIQE 81
QY 25 YLEKALN 31
DB 82 YLEKALN 88
RESULT 2
I53416
interleukin-8 homolog - mouse
C:Species: Mus sp. (mouse)
C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C:Accession: I53416
R:Jiang, W.; Zhou, P.; Kahn, S.M.; Tomita, N.; Johnson, M.D.; Weinstein, I.B.
Exp. Cell Res. 215, 284-293, 1994
A:Title: Molecular cloning of TP41, a gene whose expression is repressed by the tumo
A:Reference number: I53416; MUID:95073497; PMID:7982471

A:Accession: I53416
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-89 <RES>
A:Cross-references: GB:S74318; NID:g7863393; PIDN:AAB32650.1; PID:g7863394
C:Genetics:
A:Gene: TPAP1
C:Superfamily: beta-thromboglobulin

```

Query Match          66.98;  Score 117;  DB 2;  length 89;
Best Local Similarity 40.3%;  Pred. No. 4.8e-09;
Matches 27;  Conservative 0;  Mismatches 4;  Indels 36;  Gaps 1;

QY      1 KPVSLSYRCPCRFFG-----GGLKWIQE 24
          |||||
Db       22 KPVSLSYRCPCRFFESHLARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLWKIQE 81
          |||||

QY      25 YLEKALN 31
          |||||
Db       82 YLEKALN 88

```

RESULT 3
G01540
cytokine SDF-1-beta - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 26-Aug-1999
C;Accession: G01540
R;Spotilla, L.D.
submitted to the EMBL Data Library, October 1994
A;Reference number: G07697
A;Accession: G01540
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-93 <SPO>
A;Cross-references: EMBL:U16752; NID:g1272194; PID:g571508
C;Superfamily: beta-thromboglobulin

```

Query Match          66.9%; Score 117; DB 2; Length 93;
Best Local Similarity 40.3%; Pred. No. 5e-09;
Matches 27; Conservative 0; Mismatches 4; Indels 36; Gaps 1;

QY      1 KPVSLSYRCPCRFFGCG-----GGLKWIQE 24
          |||||
Db       22 KPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLWIOE 81
          |||||

QY      25 YLEKALN 31
          |||||
Db       82 YLEKALN 88

```

RESULT 4
I81182
cytokine - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C;Accession: I81182
R;Tashiro, K.; Tada, H.; Heilker, R.; Shirozu, M.; Nakano, T.; Honjo, T.
Science 261, 600-603, 1993
A;Title: Signal sequence trap: a cloning strategy for secreted proteins and type I mem
A;Reference number: I59582; MUID:93342488; PMID:8342023
A;Accession: I81182
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: mRNA
A;Residues: 1-93 <RES>
A;Cross-references: GB:L12030; NID:g393181; PIDN:AAA40101.1; PID:g393182
C;Genetics:
A;Gene: SDF-1-beta
C;Superfamily: beta-thromboglobulin

Query Match	66.9%;	Score 117;	DB 2;	Length 93;
Best Local Similarity	40.3%;	Pred. No. 5e-09;		
Matches 27; Conservative	0;	Mismatches 4;	Indels 36;	Gaps 11

```
QY      1 KPVSLSYRCPCRFFG-----GGKMWIOE 24  
        |||||  
        |||||  
Db      22 KPVSLSYRCPCRFFESHIAKANVHKILNTPNCALQIVARLKNNRQVCIDPKRWIOE 81  
        |||||  
QY      25 YLEKALN 31  
        |||||  
Db      82 YLEKALN 88
```

RESULT 5
T08583
cellulose synthase (EC 2.4.1.-) catalytic chain - Arabidopsis thaliana
N/Alternate names: protein T22F8.250
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 22-Oct-1999
C/Accession: T08583; T09014
R/Bevan, M.; Zimmermann, W.; Grueneisen, A.; Wandutt, R.; Bancroft, I.; Mewes, H.W.;
submitted to the Protein Sequence Database, May 1999
A/Reference number: Z16442

A;Residues: 1-1084 <BEV>
A;Cross-references: EMBL:AL050351; GSPDB:GN00062; ATSP:T22F8.250
A;Experimental source: cultivar Columbia; BAC clone T22F8
R;Arlioli, T.; Peng, L.; Betzner, A.S.; Burn, J.; Witke, W.; Herth, W.; Camilleri, C.
Science 279, 717-720, 1998
A;Title: Molecular analysis of cellulose biosynthesis in Arabidopsis.
A;Reference number: Z13745; MUID:98111412; PMID:9445479
A;Accession: T09014
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-1084 <ARI>
A;Cross-references: EMBL:AF027173; NID:g2827140; PIDN:AAC39335.1; PID:g2827141
A;Experimental source: cultivar Columbia
C;Genetics:
A;Gene: ATSP:T22F8.250; Ath-A
A;Map position: 4
A;Introns: 27/3; 156/3; 191/1; 254/2; 343/2; 458/3; 504/3; 546/3; 617/3; 708/1; 773/3
C;Keywords: cell wall synthesis; glycosyltransferase; hexosyltransferase

Query Match	34.9%;	Score 61;	DB 2;	Length 1084;
Best Local Similarity	43.5%;	Pred. No. 2.6;		
Matches	10;	Conservative	5;	Mismatches
			8;	Indels
				Gaps
				0;
QY	3	VLSYRCPCRFFGGGLKWIQY	25	
		:	:	
Db	833	IFLSRHCPIMWGYGGGLKWLRF	855	

RESULT 6
H84604
probable cellulose synthase catalytic subunit [imported] - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cross)
C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C/Accession: H84604
R;lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.
M.; Koo, H.; Mofatt, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Utayam, L.; Tallon,
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
Nature 402, 761-768, 1999
A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A/Reference number: A84420; MUID:20083487; PMID:10617197
A/Accession: H84604
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1088 <STO>
A/Cross-References: GB:AE002093; NID:g4417271; PIDN:AAD20396.1; GSPDB:GN00139
C/Genetics:
A/Gene: At2g21770
A/Map position: 2

Query Match	34.98;	Score 61;	DB 2;	Length 1088;
Best Local Similarity	43.58;	Pred. No. 2.6;		

Matches 10; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 3 VSLSYRCPCRFEGGGLKWIQ 25
: || || : ||||| :
Db 837 IFLSRHCPIMWYGGLKWLRF 859

RESULT 7

T10797
cellulose synthase (EC 2.4.1.-) catalytic chain celA1 - upland cotton
C:Species: Gossypium hirsutum (upland cotton)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C:Accession: T10797
R:Pear, J.R.; Kawagoe, Y.; Schreckengost, W.E.; Delmer, D.P.; Stalker, D.M.
Proc. Natl. Acad. Sci. U.S.A. 93, 12637-12642, 1996
A:Title: Higher plants contain homologs of the bacterial celA genes encoding the catalytic subunit of cellulose synthase
A:Reference number: 217152; MUID:97057296; PMID:8901635
A:Accession: T10797
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-974 <PEA>
A:Cross-references: EMBL:U58283; NID:g1706955; PIDN:AAB37766.1; PID:g1706956
A:Experimental source: strain Acala SJ-2; fiber
C:Genetics:
A:Gene: celA1
A:Function:
A:Description: involved in the synthesis of cellulose
C:Keywords: glycosyltransferase; hexosyltransferase

Query Match 34.6%; Score 60.5; DB 2; Length 974;
Best Local Similarity 54.5%; Pred. No. 2.8;
Matches 12; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

QY 3 VSLSYRCPCRF-FGGGLKWIQ 23
: || || : ||||| :
Db 721 IFLSRHCPIMWYGGLKWLQ 742

RESULT 8

C83345
probable class III aminotransferase PA2413 [imported] - Pseudomonas aeruginosa (strain F)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: C83345
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: C83345
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-469 <STO>
A:Cross-references: GB:AE004668; GB:AE004091; NID:g9948446; PIDN:AG05801.1; GSPDB:GN001
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA2413

Query Match 33.1%; Score 58; DB 2; Length 469;
Best Local Similarity 43.3%; Pred. No. 3.2;
Matches 13; Conservative 1; Mismatches 16; Indels 0; Gaps 0;

QY 2 PVSLSYRCPCRFEGGGLKWIQYLEKALN 31
: || || : ||||| :
Db 199 PYPYDYRCPFGLGGEAGVKANLHYLENLNLN 228

RESULT 9

T52028
cellulose synthase [imported] - Arabidopsis thaliana (fragment)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 20-Oct-2000

C:Accession: T52028

R:Joshi, C.

submitted to the EMBL Data Library, May 1998

A:Reference number: 225890

A:Accession: T52028

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1081 <JOS>

A:Cross-references: EMBL:AF062485; PIDN:AAC29067.1

Query Match 33.1%; Score 58; DB 2; Length 1081;
Best Local Similarity 47.6%; Pred. No. 6.8;
Matches 10; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 3 VSLSYRCPCRFEGGGLKWIQ 23
: || || : ||||| :
Db 831 IFLSRHCPIMWYGGLKWL 851

RESULT 10

T35594

hypothetical protein SC6G4.43c SC6G4.43c - Streptomyces coelicolor

C:Species: Streptomyces coelicolor

C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 21-Jan-2000

C:Accession: T35594

R:Saunders, D.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, August 1998

A:Reference number: 221583

A:Accession: T35594

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-233 <SAU>

A:Cross-references: EMBL:AL031317; PIDN:CAA20421.1; GSPDB:GN00070; SCOEDB:SC6G4.43c

A:Experimental source: strain A3(2)

C:Genetics:

A:Gene: SCOEDB:SC6G4.43c

C:Superfamily: hypothetical protein H10278

Query Match 32.0%; Score 56; DB 2; Length 233;
Best Local Similarity 44.0%; Pred. No. 3.2;
Matches 11; Conservative 5; Mismatches 7; Indels 2; Gaps 1;

QY 6 SYRCPCRFEGG--GGLKWIQYLEK 28
: || || | : || : : ||
Db 135 SGRIPCRRFQGHMGEPRWVKRFMEK 159

RESULT 11

T52311

isopenicillin N epimerase [validated] - Streptomyces clavuligerus

C:Species: Streptomyces clavuligerus

C:Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 20-Oct-2000

C:Accession: T52311

R:Kovacevic, S.; Tobin, M.B.; Miller, J.R.

J. Bacteriol. 172, 3952-3958, 1990

A:Title: The beta-lactam biosynthesis genes for isopenicillin N epimerase and deaceto

A:Reference number: 226033; MUID:90299822; PMID:1694525

A:Accession: T52311

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-398 <KOV>

A:Cross-references: EMBL:M32324; PIDN:AAA26714.1

C:Genetics:

A:Gene: cefD

Query Match 30.9%; Score 54; DB 2; Length 398;
Best Local Similarity 53.3%; Pred. No. 9.8;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 8 RCPCRFFGGGGLKWI 22
: || | : | || :
Db 205 RIPCDFYAGSGHKWL 219

RESULT 12

C64104
gamma-aminobutyrate aminotransferase (EC 2.6.1.-) - Haemophilus influenzae (strain Rd KM
C:Species: Haemophilus influenzae
C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 08-Oct-1999
C:Accession: C64104; JC5879
R:Flieschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A:Reference number: A64000; MUID:95350630; PMID:7542800
A:Accession: C64104
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-454 <TRIG>
A:Cross-references: GB:U32776; GB:L42023; NID:g1573969; PIDN:AAC22610.1; PID:g1573974; T
R:Ikai, H.; Yamamoto, S.
Biol. Pharm. Bull. 21, 170-173, 1998
A:Title: Two genes involved in the 1,3-diaminopropane production pathway in Haemophilus
A:Reference number: JC5879; MUID:98173550; PMID:9514614
A:Accession: JC5879
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-454 <IKA>
A:Cross-references: GB:U32776; NID:g1573969; PIDN:AAC22610.1; PID:g1573974
C:Comment: This enzyme is involved in the pathway of 1,3-diaminopropane synthesis.
C:Genetics:
A:Note: neither the complete nucleic acid sequence nor the complete translation are shown
C:Superfamily: beta-alanine-pyruvate transaminase
C:Keywords: aminotransferase; phosphoprotein; pyridoxal phosphate
F:287/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted

Query Match 30.3%; Score 53; DB 2; Length 454;
Best Local Similarity 38.5%; Pred. No. 15;
Matches 10; Conservative 3; Mismatches 13; Indels 0; Gaps 0;

QY 2 PVSLSYRCPFRFGGGLKWIQYLE 27
| :||| | | | :||| |
Db 181 PYPHYRCPFGIGGAGAKAVEQYFE 206

RESULT 13

T46814
gamma-aminobutyrate aminotransferase (EC 2.6.1.-) rhba [imported] - Rhizobium meliloti
C:Species: Rhizobium meliloti
C:Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 02-Sep-2000
C:Accession: T46814
R:Lynch, D.; O Connell, M.; O'Brien, J.
submitted to the EMBL Data Library, December 1998
A:Description: Cloning and sequence analysis of the sinorhizobium meliloti 2011 rhizobac
A:Reference number: Z24097
A:Accession: T46814
A:Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: DNA
A:Residues: 1-470 <LYN>
A:Cross-references: EMBL:AF110737; PIDN:AAD09412.1
A:Experimental source: strain 2011
C:Genetics:
A:Gene: rhba
C:Function:
A:Pathway: siderophore biosynthesis
C:Superfamily: beta-alanine-pyruvate transaminase
C:Keywords: aminotransferase

Query Match 30.3%; Score 53; DB 2; Length 470;
Best Local Similarity 43.8%; Pred. No. 16;
Matches 14; Conservative 2; Mismatches 10; Indels 6; Gaps 2;

QY 2 PVSLSYRCPFRFGGGLKWIQYLEKAL 30
| :||| | | | :||| |

Db 198 PYPHYRCP--FGGNETATLAEYFERAL 226

RESULT 14

B95419
diaminobutyrate-pyruvate transaminase (EC 2.6.1.46) Rhba [imported] - Sinorhizobium m
C:Species: Sinorhizobium meliloti
C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 02-Aug-2002
C:Accession: B95419
R:Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubier, F.; B
; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A:Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meli
A:Reference number: A95262; MUID:21396509; PMID:11481432
A:Accession: B95419
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-470 <KUR>
A:Cross-references: GB:AE006469; PIDN:AAK65916.1; PID:g14524429; GSPDB:GN00165
A:Experimental source: strain 1021, megaplasmid pSymA
R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubl
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelau
hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh,
A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A:Reference number: A96039; MUID:21368234; PMID:11474104
A:Contents: annotation
C:Genetics:
A:Gene: rhba
A:Genome: plasmid
C:Superfamily: beta-alanine-pyruvate transaminase
C:Keywords: aminotransferase

Query Match 30.3%; Score 53; DB 2; Length 470;
Best Local Similarity 43.8%; Pred. No. 16;
Matches 14; Conservative 2; Mismatches 10; Indels 6; Gaps 2;

QY 2 PVSLSYRCPFRFGGGLKWIQYLEKAL 30
| :||| | | | :||| |
Db 198 PYPHYRCP--FGGNETATLAEYFERAL 226

RESULT 15

A13489
cytochrome c-552 [imported] - Brucella melitensis (strain 16M)
C:Species: Brucella melitensis
C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 02-Apr-2002
C:Accession: A13489
R:DelVecchio, V.G.; Kapatal, V.; Redkar, R.J.; Patra, G.; Mufer, C.; Los, T.; Ivanov
; Mazur, M.; Gotsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Let
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A:Title: The genome sequence of the facultative intracellular pathogen Brucella melit
A:Reference number: AD3252; PMID:11756688
A:Accession: A13489
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-202 <KUR>
A:Cross-references: GB:AE008917; PIDN:AAL53084.1; PID:g17983947; GSPDB:GN00190
A:Experimental source: strain 16M
C:Genetics:
A:Gene: BME1903
A:Map position: 1
C:Superfamily: membrane-bound cytochrome cym; cytochrome c homology
C:Keywords: chromoprotein; heme; iron; metalloprotein
F:84/87/Binding site: heme (Cys) (covalent) #status predicted
F:88/87/Binding site: heme iron (His) (axial ligand) #status predicted
F:153/Binding site: heme iron (Met) (axial ligand) #status predicted

Query Match 28.6%; Score 50; DB 2; Length 202;
Best Local Similarity 44.0%; Pred. No. 19;
Matches 11; Conservative 2; Mismatches 12; Indels 0; Gaps 0;

Thu Oct 9 16:39:00 2003

us-09-835-107a-11.rpr

QY 6 SYRCPGRFFGGGLKWIQEYLEKAL 30
| | : | | | | : | | |
Db 117 SYSAMKEFGAAGNKWDFEHLNKL 141

Search completed: October 9, 2003, 09:21:32
Job time : 42 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 9, 2003, 09:17:41 ; Search time 22 Seconds

(without alignments)
66.265 Million cell updates/sec

Title: US-09-835-107A-11

Perfect score: 175

Sequence: 1 KPVSLSYRCPCRFFGGGGLKWIQYLEKALN 31

Scoring table: BLOSUM62

Gapor 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	117	66.9	89	1	SDF1_MOUSE	P40224 mus musculus
2	117	66.9	93	1	SDF1_FELCA	O62657 felis silve
3	117	66.9	93	1	SDF1_HUMAN	P48061 homo sapien
4	54	30.9	397	1	CEFD_STRCL	P18549 streptomyc
5	54	30.9	955	1	B3A4_RABIT	Q9gky1 oryctolagus
6	53	30.3	454	1	DAT_HAEIN	P44951 h diamincbu
7	53	30.3	470	1	RHBA_RHIME	Q9z3r2 r diamincbu
8	53	30.3	529	1	PDP2_HUMAN	Q9p2j9 homo sapien
9	52	29.7	983	1	B3A4_HUMAN	Q96q91 homo sapien
10	51	29.1	282	1	HXCC_HUMAN	P31275 homo sapien
11	50	28.6	530	1	PDP2_RAT	O88484 rattus norv
12	49	28.0	508	1	GLPK_MYCLE	Q9cb81 mycobacteri
13	49	28.0	517	1	GLPK_MYCTU	O69664 mycobacteri
14	49	28.0	557	1	TR2M_PSESS	P06617 pseudomonas
15	49	28.0	1714	1	YP93_CAEEL	Q09475 caenorhabdi
16	48.5	27.7	257	1	PEBB_PROMA	Q9k4u5 prochloroco
17	48	27.4	331	1	FCE2_MOUSE	P20693 mus musculu
18	48	27.4	593	1	VG13_BPML5	Q05219 mycobacteri
19	48	27.4	661	1	PDAT_YEAST	P40345 saccharomyc
20	48	27.4	1429	1	LI12_CAEEL	P14585 caenorhabdi
21	47.5	27.1	430	1	TCO2_MOUSE	O88968 mus musculu
22	47	26.9	203	1	SN2B_CARAU	P36978 carassius a
23	47	26.9	398	1	CEFD_NOCLA	Q03046 nocardia la
24	47	26.9	409	1	TGF3_PIG	P15203 sus scrofa
25	47	26.9	507	1	GLK2_STRCO	Q9tjm2 streptomyc
26	47	26.9	623	1	PDAT_SCHPO	O94680 schizosacch
27	46	26.3	212	1	Y010_MYCPN	P75099 mycoplasma
28	46	26.3	390	1	ACKA_MYCPN	P75245 mycoplasma
29	45.5	26.0	387	1	KR16_HSV11	Q00098 ictalurid h
30	45	25.7	351	1	KAPL_APLCA	P21901 aplysia cali
31	45	25.7	373	1	DNAJ_CAMGE	O85213 campylobact
32	45	25.7	393	1	ACKA_MYCJE	P47599 mycoplasma
33	45	25.7	577	1	YQ4B_CAEEL	Q17426 caenorhabdi

	Q9x4dm3	aquifex	pyr
34	45	25.7	SYA_AOUPY
35	45	25.7	JAK1_HUMAN
36	45	25.7	JAK1_MOUSE
37	44.5	25.4	MYTR_MITCE
38	44.5	25.4	EPG_RALSO
39	44.5	25.4	TRAZ_HUMAN
40	44.5	25.4	FAST_MOUSE
41	44	25.1	Y493_AOUAE
42	44	25.1	GLNA_MOUSE
43	44	25.1	RPI1_METKA
44	44	25.1	GLPK_XYLEA
45	44	25.1	TR2M_PANAY

ALIGNMENTS

```

RESULT 1
SDF1_MOUSE STANDARD; PRT; 89 AA.
ID SDF1_MOUSE
AC P40224;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Stromal cell-derived factor 1 precursor (SDF-1) (CXCL12) (Pre-B cell
DE growth stimulating factor) (PBSF) (12-O-tetradecanoylphorbol 13-
DE acetate repressed protein 1) (TPAR1) (Thymic lymphoma cell stimulating
DE factor) (TLSEF).
DE CXCL12 OR SDF1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94181581; PubMed=8134392;
RA Nagasawa T., Kikutani H., Kishimoto T.;
RT "Molecular cloning and structure of a pre-B-cell growth-stimulating
RT factor.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:2305-2309(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93342488; PubMed=8342023;
RA Tashiro K., Tada H., Hellker R., Shirozu M., Nakano T., Honjo T.;
RT "Signal sequence trap: a cloning strategy for secreted proteins and
RT type I membrane proteins.";
RL Science 261:600-603(1993).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=95073497; PubMed=7982471;
RA Jiang W., Zhou P., Kahn S.M., Tomita N., Johnson M.D.,
RA Weinstein I.B.;
RT "Molecular cloning of TPARI, a gene whose expression is repressed by
RT the tumor promoter 12-O-tetradecanoylphorbol 13-acetate (TPA).";
RL Exp. Cell Res. 215:284-293(1994).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=AKR/J;
RA Nomura M., Nakata Y., Uzawa A., Nose M., Akashi M., Suzuki G.;
RL Submitted (DEC.1994) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CHEMOATTRACTANT ACTIVE ON T-LYMPHOCYTES, MONOCYTES, BUT
CC NOT NEUTROPHILS.
CC -1- FUNCTION: STIMULATES THE PROLIFERATION OF BONE MARROW-DERIVED B
CC PROGENITOR CELLS IN THE PRESENCE OF IL-7 AS WELL AS GROWTH OF THE
CC STROMAL CELL-DEPENDENT B-CELL CLONE DW34 CELLS.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Alpha;
CC IsoId=P40224-1; Sequence=Displayed;
CC Name=Beta;
CC IsoId=P40224-2; Sequence=VSP_001057;
CC -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
CC C-X-C) (CHEMOKINE CXC).

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CC -----
DR EMBL; D21072; BAA04648.1; -
DR EMBL; L12029; AAA40100.1; -
DR EMBL; L12030; AAA40101.1; -
DR EMBL; S74318; AAB32650.1; -
DR EMBL; D43804; BAA07862.1; -
DR EMBL; D43805; BAA07863.1; -
DR PIR; A53497; A53497.
DR PIR; I81182; I81182.
DR HSSP; P48061; 1SDF.
DR MGD; MGI:103556; Cxcl12.
DR GO; GO:0008009; F:chemokine activity; IDA.
DR GO; GO:0007420; P:brain development; IDA.
DR GO; GO:0030334; P:regulation of cell migration; IDA.
DR InterPro; IPR001811; Chemokine_IL8.
DR InterPro; IPR001089; CXC_chmkine_sml.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00471; SMALL_CYTOKINES_CXC; FALSE_NEG.
KW Cytokine; Chemotaxis; Growth factor; Signal; Alternative splicing.
FT SIGNAL 19 POTENTIAL.
FT CHAIN 20 STROMAL CELL-DERIVED FACTOR 1.
FT DISULFID 30 BY SIMILARITY.
FT DISULFID 32 BY SIMILARITY.
FT VARSPLIC 89 K -> KRLKM (in isoform Beta).
SQ SEQUENCE 89 AA; 10032 MW; CAB8AD69078E55FA CRC64;

Query Match 66.9%; Score 117; DB 1; Length 89;
Best Local Similarity 40.3%; Pred. No. 3.4e-10;
Matches 27; Conservative 0; Mismatches 4; Indels 36; Gaps 1;

QY 1 KPVSLSYRCPCRFFGG-----GGLKWIQE 24
Db 22 KPVSLSYRCPCRFFESHARANKVHLKILNTPNCALQIVARLKNNNROYCIDPKLKWIOE 81

QY 25 YLEKALN 31
Db 82 YLEKALN 88

RESULT 2
SDF1_FELCA STANDARD; PRT; 93 AA.
ID SDF1_FELCA
AC 062657;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Stromal cell-derived factor 1 precursor (SDF-1) (CXCL12).
GN CXCL12 OR SDF1.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
RC TISSUE=Thymus;
RX MEDLINE=98450506; PubMed=9777331;
RA Nishimura Y., Miyazawa T., Ikeda Y., Izumiya Y., Nakamura K.,
RA Cai J.S., Sato E., Kohmoto M., Mikami T.;
RT "Molecular cloning and sequencing of feline stromal cell-derived
RT factor-1 alpha and beta.";
RL Eur. J. Immunogenet. 25:303-305(1998).
CC -!- FUNCTION: CHEMOATTRACTANT ACTIVE ON T-LYMPHOCYTES, MONOCYTES, BUT
CC NOT NEUTROPHILS.
```

```
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Beta;
CC IsoId=O62657-1; Sequence=Displayed;
CC Name=Alpha;
CC IsoId=O62657-2; Sequence=VSP_001055;
CC -!- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
CC C-X-C) (CHEMOKINE CXC).
CC -----
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CC -----
DR EMBL; AB011966; BAA28602.1; -
DR HSSP; P48061; 1SDF.
DR InterPro; IPR001811; Chemokine_IL8.
DR InterPro; IPR001089; CXC_chmkine_sml.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00471; SMALL_CYTOKINES_CXC; FALSE_NEG.
KW Cytokine; Chemotaxis; Growth factor; Signal; Alternative splicing.
FT SIGNAL 19 POTENTIAL.
FT CHAIN 20 STROMAL CELL-DERIVED FACTOR 1.
FT DISULFID 30 BY SIMILARITY.
FT DISULFID 32 BY SIMILARITY.
FT VARSPLIC 90 Missing (in isoform Alpha).
SQ SEQUENCE 93 AA; 10581 MW; 44FC763711E9BE37 CRC64;

Query Match 66.9%; Score 117; DB 1; Length 93;
Best Local Similarity 40.3%; Pred. No. 3.6e-10;
Matches 27; Conservative 0; Mismatches 4; Indels 36; Gaps 1;

QY 1 KPVSLSYRCPCRFFGG-----GGLKWIQE 24
Db 22 KPVSLSYRCPCRFFESHVARANKVHLKILNTPNCALQIVARLKNNNROYCIDPKLKWIOE 81

QY 25 YLEKALN 31
Db 82 YLEKALN 88

RESULT 3
SDF1_HUMAN STANDARD; PRT; 93 AA.
ID SDF1_HUMAN
AC P48061;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Stromal cell-derived factor 1 precursor (SDF-1) (CXCL12) (Pre-B cell
DE growth stimulating factor) (PBSF) (HIRH).
GN CXCL12 OR SDF1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Spotila L.D.;
RL Submitted (OCT-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96039262; PubMed=7490086;
RA Shirozu M., Nakano T., Inazawa J., Tashiro K., Tada H.,
RA Shinohara T., Honjo T.;
RT "Structure and chromosomal localization of the human stromal cell-
RT derived factor 1 (SDF1) gene.";
RL Genomics 28:495-500(1995).
CC [3]
```

RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RC TISSUE=Liver;
RA Begum N.A., Barnard G.F.;
RT "Nucleotide sequence of hIRH, human interleukin reduced in
RT hepatomas.";
RL Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.
RN [4]
RP STRUCTURE BY NMR OF 22-88.
RX MEDLINE=98046030; PubMed=9384579;
RA Crump M.P., Gong J.H., Loetscher P., Rajaratnam K., Amara A.,
RA Arenzana-Seisdedos F., Virelizier J.L., Baggiolini M., Sykes B.D.,
RA Clark-Lewis I.;
RT "Solution structure and basis for functional activity of stromal
RT cell-derived factor-1; dissociation of CXCR4 activation from binding
RT and inhibition of HIV-1.";
RL EMBO J. 16:6996-7007(1997).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 22-88.
RX MEDLINE=98284037; PubMed=9618518;
RA Dealwis C., Fernandez E.J., Thompson D.A., Simon R.J., Siani M.A.,
RA Lolis E.;
RT "Crystal structure of chemically synthesized [N33A] stromal
RT cell-derived factor 1alpha, a potent ligand for the HIV-1 'fusin'
RT coreceptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:6941-6946(1998).
CC -1- FUNCTION: CHEMOATTRACTANT ACTIVE ON T-LYMPHOCYTES, MONOCYTES, BUT
CC NOT NEUTROPHILS.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Beta;
CC IsoId=PA8061-1; Sequence=Displayed;
CC Name=Alpha;
CC IsoId=PA8061-2; Sequence=VSP_001056;
CC -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
CC C-X-C) (CHEMOKINE CXC).
CC -----
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CC -----
DR EMBL; U16752; AAA97434.1; -;
DR EMBL; L36033; AAB39332.1; -;
DR EMBL; L36034; AAB39333.1; -;
DR EMBL; U19495; AAB40516.1; -;
DR PIR; G01540; G01540.
DR PDB; 1SDF; 28-JAN-98.
DR PDB; 2SDF; 17-JUN-98.
DR PDB; 1A15; 12-AUG-98.
DR PDB; 1QG7; 28-FEB-01.
DR Genew; HGNC:10672; CXCL12.
DR MIM; 600835; -;
DR GO; GO:0003800; F:antiviral response protein activity; TAS.
DR GO; GO:0008009; F:chemokine activity; TAS.
DR GO; GO:0006874; P:calcium ion homeostasis; TAS.
DR GO; GO:0007155; P:cell adhesion; TAS.
DR GO; GO:0006935; P:chemotaxis; TAS.
DR GO; GO:0008015; P:circulation; TAS.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.
DR GO; GO:0006955; P:immune response; TAS.
DR GO; GO:0008064; P:regulation of actin polymerization and/or d. . .; TAS.
DR GO; GO:0009615; P:response to viruses; TAS.
DR GO; GO:0007165; P:signal transduction; TAS.
DR InterPro; IPR001811; Chemokine_IL8.
DR InterPro; IPR001089; CXC_chemkine_sml1.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00471; SMALL_CYTOKINES_CXC; FALSE_NEG.
KW Cytokine; Chemotaxis; Growth factor; Signal; Alternative splicing;
3D-structure.

FT SIGNAL 1 19
FT CHAIN 20 93
FT DISULFID 30 55
FT DISULFID 32 71
FT VARSPPLIC 90 93
FT
FT STRAND. 36 36
FT HELIX 41 43
FT STRAND 44 52
FT TURN 53 55
FT STRAND 56 63
FT TURN 64 66
FT STRAND 69 72
FT TURN 74 75
FT HELIX 77 85
FT TURN 86 87
SO SEQUENCE 93 AA; 10666 MW; 505B5A29C2B44E8D CRC64;

Query Match 66.9%; Score 117; DB 1; Length 93;
Best Local Similarity 40.3%; Pred. No. 3.6e-10;
Matches 27; Conservative 0; Mismatches 4; Indels 36; Gaps 1;

QY 1 KPVSLSYRCPGRFFEGG-----GGLKWIOE 24
Db 22 KPVSLSYRCPGRFFESHVARANKHLKIINTPNCALQIVARLKNNNRQVCIDPKLKWIOE 81
QY 25 YLEKALN 31
Db 82 YLEKALN 88

RESULT 4
CEFD_STRCL STANDARD; PRT; 397 AA.
ID CEFD_STRCL
AC P18549;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Isopenicillin N epimerase (EC 5.1.1.17).
GN CEFD.
OS Streptomyces clavuligerus.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxId=1901;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 27064 / DSM 738 / NRRL 3585;
RX MEDLINE=90299822; PubMed=1694525;
RA Kovacevic S., Tobin M.B., Miller J.R.;
RT "The beta-lactam biosynthesis genes for isopenicillin N epimerase and
RT deacetoxycephalosporin C synthetase are expressed from a single
RT transcript in Streptomyces clavuligerus.";
RL J. Bacteriol. 172:3952-3958(1990).
RN [2]
RP SEQUENCE OF 1-23.
RX MEDLINE=90028393; PubMed=2804141;
RA Usui S., Yu C.-A.;
RT "Purification and properties of isopenicillin N epimerase from
RT Streptomyces clavuligerus.";
RL Biochim. Biophys. Acta 999:78-85(1989).
CC -1- FUNCTION: Catalyzes the reversible isomerization between
CC isopenicillin N and penicillin N.
CC -1- CATALYTIC ACTIVITY: Isopenicillin N = penicillin N.
CC -1- COFACTOR: Pyridoxal phosphate.
CC -1- PATHWAY: Cephalosporin antibiotics biosynthesis.
CC -1- SIMILARITY: Belongs to class-V of pyridoxal-phosphate-dependent
CC aminotransferases.
CC -----
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CC -----
DR EMBL; M32324; AAA26714.1; -.
DR PIR; T52311; T52311.
DR InterPro; IPR000192; AminoTransfV.
DR Pfam; PF00266; aminoTran_5; 1.
DR PROSITE; PS00595; AA_TRANSFER_CLASS_5; 1.
KW Antibiotic biosynthesis; Isomerase; Pyridoxal phosphate.
FT INT_MET 0
FT BINDING 216 216 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
SQ SEQUENCE 397 AA; 43366 MW; A152741899F192FF CRC64;
QY 8 RCPCRFFGGGGLKWI 22
Db 204 RIPCDFYAGSGHKWL 218
-----
RESULT 5
B3A4_RABIT
ID B3A4_RABIT STANDARD; PRT; 955 AA.
AC Q9GKY1; Q9GKY2;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Anion exchange protein 4 (Anion exchanger 4).
DE SIC4A9 OR AE4.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
ON NCBI_TaxID=9986;
RX [1]
RX SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), FUNCTION, AND
RP CHARACTERIZATION.
RP TISSUE=Kidney;
RC MEDLINE=21269379; PubMed=11102437;
RA Tsuganezawa H., Kobayashi K., Iyori M., Araki T., Koizumi A.,
RA Watanabe S.-I., Kaneko A., Fukao T., Monkawa T., Yoshida T., Kim D.K.,
RA Kanai Y., Endou H., Hayashi M., Saruta T.;
RA "A new member of the HCO3-transporter superfamily is an apical anion
RT exchanger of beta-intercalated cells in the kidney.";
RL J. Biol. Chem. 276:8180-8189(2001).
CC -1- FUNCTION: Probable apical anion exchanger of the beta-intercalated
CC cells of kidney. May participate in HCO3(-) secretion.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. In contrast to
CC the rat ortholog, it is present on apical membrane of cortical
CC kidney cells.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=AE4a;
CC IsoId=Q9GKY1-1; Sequence=Displayed;
CC Name=2; Synonyms=AE4b;
CC IsoId=Q9GKY1-2; Sequence=VSP_007088;
CC -1- TISSUE SPECIFICITY: Highly expressed in kidney. Expressed in
CC certain types of cells in the kidney cortex.
CC -1- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
CC -----
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CC -----
DR EMBL; AB038263; BAB18935.1; -
DR EMBL; AB038264; BAB18936.1; -
DR HSP; P02730; IBNX.
DR InterPro; IPR001717; Anion_exchange.

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DR InterPro; IPR003020; HCO3_cotransp.
DR Pfam; PF00955; HCO3_cotransp; 1.
DR PRINTS; PR01231; HCO3TRNSPORT.
DR TIGRFAMs; TIGR00834; ae; 1.
KW Transmembrane; Glycoprotein; Transport; Antiport; Ion transport;
KW Anion exchange; Alternative splicing.
FT DOMAIN 1 386 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 387 955 MEMBRANE (ANION EXCHANGE).
FT TRANSMEM 387 407 POTENTIAL.
FT TRANSMEM 415 435 POTENTIAL.
FT TRANSMEM 438 458 POTENTIAL.
FT TRANSMEM 472 492 POTENTIAL.
FT TRANSMEM 503 523 POTENTIAL.
FT DOMAIN 524 595 EXOPLASMIC LOOP (POTENTIAL).
FT TRANSMEM 596 616 POTENTIAL.
FT TRANSMEM 637 657 POTENTIAL.
FT DOMAIN 658 683 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 684 704 POTENTIAL.
FT TRANSMEM 730 750 POTENTIAL.
FT TRANSMEM 785 804 POTENTIAL.
FT TRANSMEM 847 867 POTENTIAL.
FT TRANSMEM 871 891 POTENTIAL.
FT CARBOHYD 548 548 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 572 572 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 317 332 Missing (in isoform 2).
FT SEQUENCE 955 AA; 105032 MW; 04E595A2BFC415B7 CRC64;

Query Match 30.9%; Score 54; DB 1; Length 955;
Best Local Similarity 55.6%; Pred. No. 5.4;
Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps

Oy 1 KPVSLSYRCPCRFGGG 18
   : 11:11111111
Db 530 RFGSLAYGCLCQFPFGG 547

RESULT 6
DAT_HAEIN
ID DAT_HAEIN STANDARD; PRT; 454 AA.
AC P44951;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Diaminobutyrate-2-oxoglutarate aminotransferase (EC 2.6.1.76) (L-
DE diaminobutyric acid transaminase) (Diaminobutyrate transaminase) (DABA
DE aminotransferase) (DABA-AT) (L-2,4-diaminobutyrate:2-ketoglutarate 4-
DE aminotransferase).
GN DAT OR HI0949.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
CX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Rd / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA Mckenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Usterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fitchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RA "Whole-genome random sequencing and assembly of Haemophilus influenzae
RT Rd.";
RL Science 269:496-512(1995).
RN [2]
RP CHARACTERIZATION.
RX MEDLINE=98173550; PubMed=9514614;
RA Ikai H., Yamamoto S.;

```


RT "Two genes involved in the 1,3-diaminopropane production pathway in
RL Haemophilus influenzae.";
CC Biol. Pharm. Bull. 21:170-173(1998).
CC -1- CATALYTIC ACTIVITY: L-2,4-diaminobutyrate + 2-oxoglutarate = L-
CC glutamate + L-aspartic 4-semialdehyde.
CC -1- COFACTOR: Pyridoxal phosphate (potential).
CC -1- PATHWAY: 1,3-diaminopropane biosynthesis.
CC -1- SIMILARITY: Belongs to class-III of pyridoxal-phosphate-dependent
CC aminotransferases.
CC -----
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CC -----
DR EMBL; U32776; AAC22610.1; -.
DR PIR; C64104; C64104.
DR HSSP; P12995; 10J3.
DR TIGR; HI0949; -.
DR InterPro; IPR005814; Aminotrans_3.
DR InterPro; IPR004637; Dat.
DR Pfam; PF00202; aminotran_3; 1.
DR TIGRFAMS; TIGR00709; dat; 1.
DR PROSITE; PS00600; AA_TRANSFER_CLASS_3; 1.
KM Transferase; Aminotransferase; Pyridoxal phosphate; Complete proteome.
FT BINDING 287 287 PYRIDOXAL PHOSPHATE (POTENTIAL).
SQ SEQUENCE 454 AA; 49368 MW; B4B26F3AB7C55063 CRC64;

Query Match 30.3%; Score 53; DB 1; Length 454;
Best Local Similarity 38.5%; Pred. NO. 3.6;
Matches 10; Conservative 3; Mismatches 13; Indels 0; Gaps 0;

QY 2 PVSLSYRCPCRFPGGGGLKWIQYLE 27
Db 181 PYPHEYRCPCFGIGEGAGAKAVEQYFE 206
ID RHBA_RHIME STANDARD; PRT; 470 AA.
AC Q923R2;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Diaminobutyrate--2-oxoglutarate aminotransferase (EC 2.6.1.76) (L-
DE diaminobutyric acid transaminase) (Diaminobutyrate transaminase) (DABA
DE aminotransferase) (DABA-AT) (L-2,4-diaminobutyrate:2-Ketoglutarate 4-
DE aminotransferase).
GN RHBA OR RHSA OR RA1258 OR SMA2400.
OS Rhizobium meliloti (Sinorhizobium meliloti).
OG Plasmid pSymba (megaplasmid 1).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21172875; PubMed=11274118;
RA Lynch D., O'Brien J., Welch T., Clarke P., Cui P.O., Crosa J.H.,
RA O'Connell M.;
RA "Genetic organization of the region encoding regulation, biosynthesis,
RA and transport of rhizobactin 1021, a siderophore produced by
RT Sinorhizobium meliloti";
RL J. Bacteriol. 183:2576-2585(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21396509; PubMed=11481432;
RA Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,
RA Barloy-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J.,

RA Gurjal M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L.,
RA Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,
RA Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.,
RT "Nucleotide sequence and predicted functions of the entire
RT Sinorhizobium meliloti pSymba megaplasmid";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888(2001).
CC -1- CATALYTIC ACTIVITY: L-2,4-diaminobutyrate + 2-oxoglutarate = L-
CC glutamate + L-aspartic 4-semialdehyde.
CC -1- COFACTOR: Pyridoxal phosphate.
CC -1- PATHWAY: Rhizobactin siderophore biosynthesis.
CC -1- SIMILARITY: Belongs to class-III of pyridoxal-phosphate-dependent
CC aminotransferases.
CC -----
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CC -----
DR EMBL; AF110737; AAD09412.1; -.
DR EMBL; AE007311; AAK65916.1; -.
DR PIR; B95419; B95419.
DR PIR; T46814; T46814.
DR HSSP; P12995; 10J3.
DR InterPro; IPR005814; Aminotrans_3.
DR InterPro; IPR004637; Dat.
DR Pfam; PF00202; aminotran_3; 1.
DR TIGRFAMS; TIGR00709; dat; 1.
DR PROSITE; PS00600; AA_TRANSFER_CLASS_3; 1.
KM Transferase; Aminotransferase; Pyridoxal phosphate; Iron transport;
KW Plasmid; Complete proteome.
FT BINDING 304 304 PYRIDOXAL PHOSPHATE (POTENTIAL).
SQ SEQUENCE 470 AA; 50148 MW; 0377B3B8B9A09049 CRC64;

Query Match 30.3%; Score 53; DB 1; Length 470;
Best Local Similarity 43.8%; Pred. NO. 3.8;
Matches 14; Conservative 2; Mismatches 10; Indels 6; Gaps 2;

QY 2 PVSLSYRCPCRFPGGG--LKWIEYLEKAL 30
Db 198 PYPYATRCPC--FGRGNETATLAIEYFERAL 226
ID PDP2_HUMAN STANDARD; PRT; 529 AA.
AC Q9P2J9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE [Pyruvate dehydrogenase (liponamide)]-phosphatase 2, mitochondrial
DE precursor (EC 3.1.3.43) (PDP 2) (Pyruvate dehydrogenase phosphatase,
DE catalytic subunit 2) (PDP2 2).
GN PDP2 OR KIAA1348.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=20181126; PubMed=10718198;
RA Nagase T., Kikuno R., Ishikawa K.-I., Hirose M., Ohara O.,
RT "Prediction of the coding sequences of unidentified human genes. XVI.
RT The complete sequences of 150 new cDNA clones from brain which code
RT for large proteins in vitro";
RL DNA Res. 7:65-73(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Yoshizuki S., Carninci P., Prange C.,
RA Bork S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzay D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- FUNCTION: CATALYZES THE DEPHOSPHORYLATION AND CONCOMITANT
CC REACTIVATION OF THE ALPHA SUBUNIT OF THE E1 COMPONENT OF THE
CC PYRUVATE DEHYDROGENASE COMPLEX (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: [pyruvate dehydrogenase (lipoamide)] phosphate
CC + H(2)O = [pyruvate dehydrogenase (lipoamide)] + phosphate.
CC -1- COFACTOR: MAGNESIUM DEPENDENT (BY SIMILARITY).
CC -1- SUBUNIT: HETERODIMER OF A CATALYTIC SUBUNIT AND A FAD PROTEIN OF
CC UNKNOWN FUNCTION (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix (By similarity).
CC -1- SIMILARITY: BELONGS TO THE PP2C FAMILY.
CC -----
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CC -----
DR EMBL; AB037769; BAA92586.1; ALT_INIT.
DR EMBL; BC028030; AAH28030.1; -.
DR InterPro; IPR001932; PP2C-like.
DR InterPro; IPR000222; PP2C.
DR Pfam; PF00481; PP2C; 2.
DR SMART; SM00331; PP2C_SIG; 1.
DR SMART; SM00332; PP2C; 1.
DR PROSITE; PS01032; PP2C; 1.
KW Hydroxylase; Mitochondrion; Transit peptide; Magnesium.
FT TRANSIT 1 66 MITOCHONDRION (POTENTIAL).
FT CHAIN 67 529 [PYRUVATE DEHYDROGENASE [LIPOMIDE]]-
FT PHOSPHATASE 2.
SQ SEQUENCE 529 AA; 59978 MW; 252CABCDADF61A5C CRC64;
Query Match 30.3%; Score 53; DB 1; Length 529;
Best Local Similarity 46.2%; Pred. No. 4.2;
Matches 12; Conservative 2; Mismatches 8; Indels 4; Gaps 1;
QY 10 PCRFFGGGGLKWKIQE---YLEKALN 31
DQ 344 PCRAFGDVQLKWSKELQRLERGFN 369
RESULT 9
B3A4_HUMAN STANDARD; PRT; 983 AA.
ID B3A4_HUMAN
AC O96Q91; O96RM5; O9BXF2; O9BXN3;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Anion exchange protein 4 (Anion exchanger 4) (Sodium bicarbonate
DE cotransporter 5).
GN SLC4A9 OR AE4 OR SBC5.
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Kidney and Testis;
RX MEDLINE=21199380; PubMed=11302728;
RA Parker M.D., Ourmozdi E.P., Tanner M.J.A.;
RT "Human BTRL, a new bicarbonate transporter superfamily member and
RT human AE4 from kidney."
RL Biochem. Biophys. Res. Commun. 282:1103-1109(2001).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND TISSUE SPECIFICITY.
RC TISSUE=Kidney;
RX MEDLINE=21204185; PubMed=11305939;
RA Lipovich L., Lynch E.D., Lee M.K., King M.-C.;
RT "A novel sodium bicarbonate cotransporter-like gene in an ancient
RT duplicated region: SLC4A9 at 5q31."
RL Genome Biol. 2:RESEARCH0011.1-RESEARCH0011.13(2001).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RA Karet F.E.;
RT "Cloning and characterization of human AE4."
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 3-983 FROM N.A. (ISOFORM 3), AND TISSUE SPECIFICITY.
RC TISSUE=Testis;
RA Ishibashi K.;
RT "Molecular cloning of human sodium bicarbonate cotransporter 5."
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [5]
RP FUNCTION: Probable apical anion exchanger of the kidney cortex (By
RP similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=3;
CC Name=1;
CC IsoId=Q96Q91-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q96Q91-2; Sequence=VSP_007085, VSP_007086, VSP_007087;
CC Name=3;
CC IsoId=Q96Q91-3; Sequence=VSP_007085;
CC -1- TISSUE SPECIFICITY: Kidney-specific.
CC -1- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
CC -----
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CC -----
DR EMBL; AF332961; AAK69625.1; -.
DR EMBL; AF336237; AAK16733.1; -.
DR EMBL; AF313465; AAK28832.1; ALT_INIT.
DR EMBL; AB032762; BAA93010.1; -.
DR HSSP; P02730; IBNX.
DR Genew; HGNC:11035; SLC4A9.
DR InterPro; IPR001717; Anion_exchanger.
DR InterPro; IPR003020; HCO3_cotransp.
DR Pfam; PF00955; HCO3_cotransp; 1.
DR PRINTS; PR01231; HCO3TRANSPRT.
DR TIGRFAMs; TIGR00834; ae; 1.
KW Transmembrane; Glycoprotein; Transport; Antipor; Ion transport;
KW Anion exchange; Alternative splicing.
FT DOMAIN 1 414 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 1 414 MEMBRANE (ANION EXCHANGE).
FT TRANSMEM 415 983 POTENTIAL.
FT TRANSMEM 415 435 POTENTIAL.
FT TRANSMEM 443 463 POTENTIAL.
FT TRANSMEM 465 485 POTENTIAL.
FT TRANSMEM 500 520 POTENTIAL.
FT TRANSMEM 530 550 POTENTIAL.
FT DOMAIN 552 623 EXOPLASMIC LOOP (POTENTIAL).

```

FT TRANSMEM 624 644 POTENTIAL.
FT TRANSMEM 665 685 POTENTIAL.
FT DOMAIN 686 711 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 712 732 POTENTIAL.
FT TRANSMEM 758 778 POTENTIAL.
FT TRANSMEM 815 835 POTENTIAL.
FT TRANSMEM 837 857 POTENTIAL.
FT TRANSMEM 899 919 POTENTIAL.
FT CARBOHYD 576 576 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 600 600 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 77 100 Missing (in isoform 2 and isoform 3).
FT VARSPLIC 384 394 Missing (in isoform 2).
FT VARSPLIC 592 594 Missing (in isoform 2).
FT VARSPLIC 592 594 Missing (in isoform 2).
FT CONFLICT 101 101 /FTid=VSP_007087.
FT CONFLICT 453 453 R -> T (IN REF. 3).
FT CONFLICT 795 795 V -> M (IN REF. 1).
SQ SEQUENCE 983 AA; 108247 MW; E2AEB04C9D27E6BC CRC64;

Query Match 29.7%; Score 52; DB 1; Length 983;
Best Local Similarity 44.0%; Pred. No. 11;
Matches 11; Conservative 5; Mismatches 7; Indels 2; Gaps 1;

QY 1 KPVSLSYRCPGRFFGGG--LKWIQ 23
DB 558 KPGSSAYGCLCQYPPGNGESQWIR 582

RESULT 10
HXCC_HUMAN STANDARD; PRT; 282 AA.
ID HXCC_HUMAN STANDARD; PRT; 282 AA.
AC P31275; Q9BXJ6;
DT 01-JUL-1993 (Rel. 26, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Homeobox protein Hox-C12 (Hox-3F).
GN HOXC12 OR HOX3F.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kosaki K., Kosaki R., Suzuki T., Yoshihashi H., Sasaki K., Matsuo N.;
RT "A complete mutation analysis panel of human HOX genes.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE OF 214-279 FROM N.A.
RX MEDLINE=90098876; PubMed=2574852;
RA Acampora D., D'Esposito M., Fatella A., Pannese M., Migliaccio E.,
RA Morelli F., Stonaiuolo A., Nigro V., Simeone A., Boncinelli E.;
RT "The human HOX gene family.";
RL Nucleic Acids Res. 17:10385-10402(1989).
CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: BELONGS TO THE ABD-B HOMEOBOX FAMILY.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF328962; AAK16717.1; -
CC EMBL; AF328963; AAK16717.1; JOINED.
CC PIR; S14933; S14933.
CC HSSP; P14653; 1B72.

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DR TRANSFAC; T03329; -
DR Genew; HGNC:5124; HOXC12.
DR MIM; 142975; -
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PR00024; HOMEBOX.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS50071; HOMEBOX_2; 1.
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KW Transcription regulation.
FT DNA_BIND 214 273 HOMEBOX.
SQ SEQUENCE 282 AA; 30171 MW; 493C53C511054A4D CRC64;

Query Match 29.1%; Score 51; DB 1; Length 282;
Best Local Similarity 37.8%; Pred. No. 4.5;
Matches 14; Conservative 1; Mismatches 4; Indels 18; Gaps 1;

QY 2 PVSLS-----YRCPGRFFGGGGLK 20
DB 72 PVSLNPPFGRTCELARVEDGKGYRPPCAEGGGGLK 108

RESULT 11
PDP2_RAT STANDARD; PRT; 530 AA.
ID PDP2_RAT STANDARD; PRT; 530 AA.
AC O88484;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE [Pyruvate dehydrogenase [lipamide]]-phosphatase 2, mitochondrial
DE precursor (EC 3.1.3.43) (PDP 2) (Pyruvate dehydrogenase phosphatase,
DE catalytic subunit 2) (PDP 2).
GN PDP2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=96316337; PubMed=9651365;
RA Huang B., Gudi R., Wu P., Harris R.A., Hamilton J., Popov K.M.;
RT "Isoenzymes of pyruvate dehydrogenase phosphatase. DNA-derived amino
RT acid sequences, expression, and regulation.";
RL J. Biol. Chem. 273:17680-17688(1998).
CC -1- FUNCTION: CATALYZES THE DEPHOSPHORYLATION AND CONCOMITANT
CC REACTIVATION OF THE ALPHA SUBUNIT OF THE E1 COMPONENT OF THE
CC PYRUVATE DEHYDROGENASE COMPLEX.
CC -1- CATALYTIC ACTIVITY: [Pyruvate dehydrogenase (lipamide)] phosphate
CC + H(2)O = [Pyruvate dehydrogenase (lipamide)] + phosphate.
CC -1- COFACTOR: MAGNESIUM.
CC -1- SUBUNIT: HETERODIMER OF A CATALYTIC SUBUNIT AND A FAD PROTEIN OF
CC UNKNOWN FUNCTION (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN LIVER.
CC -1- SIMILARITY: BELONGS TO THE PDP2 FAMILY.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF062741; AAC40168.1; -
CC InterPro; IPR001932; PDP2-like.
CC InterPro; IPR000222; PDP2.
CC Pfam; PF00481; PDP2; 2.
CC SMART; SM00331; PDP2_SIG; 1.
CC SMART; SM00332; PDP2C; 1.

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DR PROSITE; PS01032; PR2C; 1.
 KW Hydrolyase; Mitochondrion; Transit peptide; Magnesium.
 FT TRANSIT 1 67 MITOCHONDRION (POTENTIAL).
 FT CHAIN 68 530 [PYRUVATE DEHYDROGENASE [LIPOMIDE]] -
 FT PHOSPHATASE 2.
 SQ SEQUENCE 530 AA; 59654 MW; 5AB688FAC78AD9CD CRC64;
 Query Match 28.6%; Score 50; DB 1; Length 530;
 Best Local Similarity 47.6%; Pred. No. 12;
 Matches 10; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 10 PCRFFGGGGLKWIQYLEKAL 30
 ||| || ||| :|
 Db 345 PCRAFGDVQLKWSKELQRNVL 365

RESULT 12
 GLPK_MYCLE STANDARD; PRT; 508 AA.
 AC O9CB81;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Glycerol kinase (EC 2.7.1.30) (ATP:glycerol 3-phosphotransferase)
 DE (Glycerokinase) (GK).
 GN GLPK OR ML2314.
 OS Mycobacterium leprae.
 OC Bacteria; Actinobacteria; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1769;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TN;
 RX MEDLINE=21128732; PubMed=11234002;
 RA Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,
 RA Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
 RA Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
 RA Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
 RA Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
 RA Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
 RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
 RA Barrell B.G.;
 RA "Massive gene decay in the leprosy bacillus.";
 RL Nature 409:1007-1011(2001).
 CC -1- FUNCTION: KEY ENZYME IN THE REGULATION OF GLYCEROL UPTAKE AND
 CC METABOLISM.
 CC -1- CATALYTIC ACTIVITY: ATP + glycerol = ADP + glycerol 3-phosphate.
 CC -1- PATHWAY: Glycerol utilization; rate-limiting step.
 CC -1- SIMILARITY: BELONGS TO THE FUCOKINASE / GLUCONOKINASE /
 CC GLYCEROKINASE / XYLUOKINASE FAMILY.
 CC -----
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 CC -----
 CC EMBL; AL583925; CAC31830.1; -
 CC PIR; F87198; F87198.
 CC HSSP; P08859; IGLC.
 CC Leproma; ML2314; -
 CC HAMAP; MF_00186; -; 1.
 CC InterPro; IPR000577; FGGY_kin.
 CC InterPro; IPR005999; Glycerol_kin.
 CC Pfam; PF00370; FGGY; 1.
 CC Pfam; PF02782; FGGY_C; 1.
 CC TIGRFAMS; TIGR01311; glycerol_kin; 1.
 CC PROSITE; PS00933; FGGY_KINASES_1; 1.
 CC PROSITE; PS00445; FGGY_KINASES_2; 1.
 KW Glycerol metabolism; Transferase; Kinase; ATP-binding;

KW Complete proteome.
 FT NP_BIND 156 168 ATP (PROBABLE).
 SQ SEQUENCE 508 AA; 54658 MW; A15379793ECF4039 CRC64;
 Query Match 28.0%; Score 49; DB 1; Length 508;
 Best Local Similarity 44.4%; Pred. No. 16;
 Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 10 PCRFFGGGGLKWIQYLE 27
 | : | | | : | : | :
 Db 134 PATYFSGGKLQWILENVD 151

RESULT 13
 GLPK_MYCTU STANDARD; PRT; 517 AA.
 ID GLPK_MYCTU
 AC O69664;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Glycerol kinase (EC 2.7.1.30) (ATP:glycerol 3-phosphotransferase)
 DE (Glycerokinase) (GK).
 GN GLPK OR RV3696C OR MTW025.044C.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Actinobacteria; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H37RV;
 RX MEDLINE=98295987; PubMed=9634230;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
 RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutter S., Seeger K., Skelton J., Squares R.,
 RA Sulston J.B., Taylor K., Whitehead S., Barrell B.G.;
 RA "Deciphering the biology of Mycobacterium tuberculosis from the
 RA complete genome sequence.";
 RL Nature 393:537-544(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CDC 1551 / Oshkosh;
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 RA Peterson J., DeBoy R., Dodson R., Gwin M.L., Haft D., Hickey E.,
 RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
 RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
 RA Bishai W.;
 RA "Whole genome comparison of Mycobacterium tuberculosis clinical and
 RA laboratory strains.";
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: KEY ENZYME IN THE REGULATION OF GLYCEROL UPTAKE AND
 CC METABOLISM.
 CC -1- CATALYTIC ACTIVITY: ATP + glycerol = ADP + glycerol 3-phosphate.
 CC -1- PATHWAY: Glycerol utilization; rate-limiting step.
 CC -1- SIMILARITY: BELONGS TO THE FUCOKINASE / GLUCONOKINASE /
 CC GLYCEROKINASE / XYLUOKINASE FAMILY.
 CC -----
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 CC -----
 CC EMBL; AL022121; CA18018.1; -
 CC EMBL; AE007177; AAK48165.1; -
 CC PIR; A70793; A70793.
 CC HSSP; P08859; IGLC.
 CC TIGR; MT3798; -


```
DR Tuberculin; RV3696C; -.
DR HAMAP; ME_00186; -. 1.
DR InterPro; IPR000577; FGcy_kin.
DR InterPro; IPR005999; Glycerol_kin.
DR Pfam; PF00370; FGcy_1.
DR Pfam; PF02782; FGcy_C; 1.
DR TIGRfams; TIGR01311; glycerol_kin; 1.
DR PROSITE; PS00445; FGcy_KINASES_2; 1.
DR PROSITE; PS00933; FGcy_KINASES_1; 1.
DR Glycerol metabolism; Transferase; Kinase; ATP-binding;
KW Complete proteome.
FT NP_BIND 165 177 ATP (PROBABLE).
SQ SEQUENCE 517 AA; 55859 MW; 7E3F30DCF2A1E63E CRC64;

Query Match
Best Local Similarity 28.0%; Score 49; DB 1; Length 517;
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 10 PCRFEGGGGLKWIQYLE 27
   | | | | | | | | | |
Db 143 PATYFSGGKIQWILENVD 160
```

```
RESULT 14
TR2M_PSESS STANDARD; PRT; 557 AA.
ID TR2M_PSESS
AC P06617;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Tryptophan 2-monooxygenase (EC 1.13.12.3).
GN IAM.
OS Pseudomonas syringae (pv. savastanoi).
OG Plasmid pIA1.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=29438;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EW2009;
RA Yamada T., Palm C.J., Brooks B., Kosuge T.;
RT "Nucleotide sequences of the Pseudomonas savastanoi indoleacetic acid
   genes show homology with Agrobacterium tumefaciens T-DNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:6522-6526(1985).
CC -1- CATALYTIC ACTIVITY: L-tryptophan + O(2) = indole-3-acetamide +
   CO(2) + H(2)O.
CC -1- PATHWAY: Biosynthesis of auxins from tryptophan; first step.
CC -----
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CC -----
CC EMBL; M11035; AAA25852.1; -.
DR PIR; A25493; A25493.
DR InterPro; IPR000759; Adrndx_reductase.
DR InterPro; IPR002937; Amino_oxidase.
DR InterPro; IPR000205; NAD_binding.
DR Pfam; PF01593; Amino_oxidase; 1.
DR PRINTS; PR00419; ADXRDTASE.
KW Plasmid; Oxidoreductase; Monooxygenase; Auxin biosynthesis.
SQ SEQUENCE 557 AA; 61861 MW; A3EA5CF7B4A94289 CRC64;
```

```
Query Match
Best Local Similarity 28.0%; Score 49; DB 1; Length 557;
Matches 10; Conservative 3; Mismatches 6; Indels 4; Gaps 1;

QY 9 PCRFEGGGGLKWIQYLEKALN 31
   | | | | | | | | | |
Db 511 CSCSFAGG----WIEGAVQTALN 529
```

```
RESULT 15
YP93_CAEEL STANDARD; PRT; 1714 AA.
ID YP93_CAEEL
AC Q09475;
DT 01-NOV-1995 (Rel. 32, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Putative helicase C28H8.3 (EC 3.6.1.-).
DE C28H8.3.
GN Caenorhabditis elegans.
OS Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Miller N., Waterston R.;
RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP REVISIONS.
RA Waterston R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -1- SIMILARITY: BELONGS TO THE HELICASE FAMILY. SKI2 SUBFAMILY.
CC -----
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CC -----
CC EMBL; U20861; AAA62291.2; -.
DR WormPep; C28H8.3; CE29195.
DR InterPro; IPR001410; DEAD.
DR InterPro; IPR001650; Helicase_C.
DR Pfam; PF00271; DEAD; 1.
DR Pfam; PF00271; helicase_C; 1.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELIC; 1.
KW Hypothetical protein; Hydrolase; Helicase; ATP-binding;
KW Nuclear protein.
FT NP_BIND 607 614 ATP (POTENTIAL).
FT NP_BIND 806 813 ATP (POTENTIAL).
FT SITE 913 916 DEVI BOX.
FT SITE 913 916
SQ SEQUENCE 1714 AA; 194095 MW; 0936764D27C7EFAD CRC64;
```

```
QY 10 PCRFEGGGGLK--WQ----EYLEKAL 30
   | | | | | | | | | |
Db 1058 PCKFFGQHGTKAVWISRSRLRLLENAL 1084
```

Search completed: October 9, 2003, 09:18:15
Job time : 25 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 9, 2003, 09:17:42 ; Search time 95 Seconds

(without alignments)
84.207 Million cell updates/sec

Title: US-09-835-107A-11

Perfect score: 175
Sequence: 1 KPVSLSYRCPCRFFGGGLKWIQYLEKALN 31

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_23:*
1: sp-archaea:*
2: sp-bacteria:*
3: sp-fungi:*
4: sp-human:*
5: sp-invertebrate:*
6: sp-mammal:*
7: sp-mhc:*
8: sp-organelle:*
9: sp-phage:*
10: sp-plant:*
11: sp-rodent:*
12: sp-virus:*
13: sp-vertebrate:*
14: sp-unclassified:*
15: sp-virus:*
16: sp-bacteriap:*
17: sp-archeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	117	66.9	89	6	Q8HYPO	Q8HYPO macaca mula
2	117	66.9	92	4	Q9H554	Q9H554 homo sapien
3	114	65.1	89	11	Q9QZD1	Q9QZD1 rattus norv
4	105	60.0	94	13	Q8UWJ9	Q8UWJ9 xenopus lae
5	61	34.9	507	10	Q93YP8	Q93YP8 arabidopsis
6	61	34.9	1084	10	Q48947	Q48947 arabidopsis
7	61	34.9	1088	10	Q9SJ22	Q9SJ22 arabidopsis
8	60.5	34.6	974	10	P93155	P93155 gossypium h
9	60.5	34.6	974	10	Q8W1W0	Q8W1W0 gossypium h
10	58	33.1	346	10	Q8L778	Q8L778 arabidopsis
11	58	33.1	366	10	Q94JU6	Q94JU6 arabidopsis
12	58	33.1	469	16	Q91168	Q91168 pseudomonas
13	58	33.1	1069	10	Q9F1B9	Q9F1B9 arabidopsis
14	58	33.1	1081	10	O65338	O65338 arabidopsis
15	58	33.1	1084	10	Q9FGF9	Q9FGF9 arabidopsis
16	57.5	32.9	939	10	Q943H3	Q943H3 oryza sativ

17	57	32.6	424	5	Q8FKT6	Q8FKT6 escherichia
18	57	32.6	978	10	Q9VCS4	Q9VCS4 drosophila
19	56.5	32.3	233	16	O81368	O81368 populus tre
20	56	32.0	422	5	O86804	O86804 streptomyce
21	54	30.9	939	6	Q9GUY1	Q9GUY1 caenorhabdi
22	54	30.9	955	6	Q9GKY2	Q9GKY2 oryctolagus
23	54	30.6	99	13	Q8AV10	Q8AV10 brachydanio
24	53.5	30.6	141	4	Q8N796	Q8N796 homo sapien
25	52.5	30.0	220	5	Q8T4G9	Q8T4G9 drosophila
26	52	29.7	945	4	Q9BXF2	Q9BXF2 homo sapien
27	52	29.7	957	4	Q96Q91	Q96Q91 homo sapien
28	52	29.7	959	4	Q96RMS	Q96RMS homo sapien
29	52	29.7	990	4	Q9BXN3	Q9BXN3 homo sapien
30	52	29.7	1063	10	Q9AV71	Q9AV71 oryza sativ
31	52	29.7	280	11	Q8K5B8	Q8K5B8 mus musculu
32	51	29.1	322	5	Q8SS28	Q8SS28 encephalito
33	51	29.1	353	5	Q9NBJ2	Q9NBJ2 drosophila
34	51	29.1	366	5	Q9NBJ1	Q9NBJ1 drosophila
35	51	29.1	959	16	Q8D8D0	Q8D8D0 vibrio vuln
36	51	29.1	1440	5	Q20204	Q20204 caenorhabdi
37	51	29.1	392	2	O07470	O07470 rhodospseudo
38	50.5	28.9	527	17	Q8PYH3	Q8PYH3 methanosarc
39	50.5	28.9	729	17	Q8TIW4	Q8TIW4 methanosarc
40	50.5	28.9	202	16	Q8YEH5	Q8YEH5 bruceella me
41	50	28.6	202	16	Q8G3B1	Q8G3B1 drosophila
42	50	28.6	202	16	Q9NBJ3	Q9NBJ3 drosophila
43	50	28.6	366	5	P93156	P93156 gossypium h
44	50	28.6	685	10	Q9SUH7	Q9SUH7 arabidopsis
45	49.5	28.3	170	10		

ALIGNMENTS

RESULT 1
Q8HYPO ID Q8HYPO PRELIMINARY; PRT; 89 AA.
AC Q8HYPO: 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Chemokine CXCL12/SDF-1ALPHA.
OS Macaca mulatta (Rhesus macaque).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
CC Cercopitheidae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Basu S., Schaefer T.M., Ghosh M., Fuller C.L., Reinhart T.A.;
RT "Comprehensive cloning and sequencing reveals evolutionary
RT conservation among all groups of rhesus macaque chemokines";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF449283; AAN76086.1; -
SQ SEQUENCE 89 AA; 10105 MW; AD5316336DC2B07 CRC64;

Query Match

Score 117; DB 6; Length 89;

Best Local Similarity 40.3%; Pred. NO. 1.5e-09;
Matches 27; Conservative 0; Mismatches 4; Indels 36; Gaps 1;

QY	1 KPVSLSYRCPCRFFG	-----GGLKWIQ 24
Db	22 KPVSLSYRCPCRFFSHVARANKLKLINPNCALQIVARLKNKNROYCIDPKLWIOE 81	
QY	25 YLEKALN 31	
Db	82 YLEKALN 88	
RESULT 2		
Q9H554 ID Q9H554 PRELIMINARY; PRT; 92 AA.		
AC Q9H554;		

```
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE BA20J15.1.2 (Stromal cell-derived factor 1, isoform beta)
DE (Fragment).
GN SDF1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Bird C.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL137026; CAC10202.1; -.
DR HSSP; P48061; 1SDF.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
FT NON_TER
SQ SEQUENCE 92 AA; 10510 MW; AEF0C402B4E8D20 CRC64;

Query Match 66.9%; Score 117; DB 4; Length 92;
Best Local Similarity 40.3%; Pred. No. 1.6e-09;
Matches 27; Conservative 0; Mismatches 4; Indels 36; Gaps 1;

QY 1 KPVSLSYRCPCRFEGG-----GGLKWIOE 24
Db 22 KPVSLSYRCPCRFESHVARANKHLKILNTPNCALQIVARLKNNGVCIDPKLKWIOE 81
QY 25 YLEKALN 31
Db 82 YLEKALN 88

RESULT 3
Q9QZD1 PRELIMINARY; PRT; 89 AA.
ID Q9QZD1
AC Q9QZD1;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE Stromal cell-derived factor-1 alpha.
GN SDF-1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RA Ohtani Y., Okada M., Kawaguchi N., Minami M., Satoh M.;
RT "cDNA cloning of rat stromal cell-derived factor-1 alpha (SDF-1
alpha).";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Pillarissetti K., Gupta S.K.;
RT "Identification and molecular cloning of a novel rat ortholog of the
alpha chemokine, stromal cell derived factor-1 (SDF-1).";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF189724; AAF01066.1; -.
DR EMBL; AF209976; AAG43506.1; -.
DR HSSP; P48061; 1SDF.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
SQ SEQUENCE 89 AA; 9977 MW; D86977626A2E35FA CRC64;

Query Match 65.1%; Score 114; DB 11; Length 89;
Best Local Similarity 38.8%; Pred. No. 4.2e-09;
Matches 26; Conservative 1; Mismatches 4; Indels 36; Gaps 1;
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QY 1 KPVSLSYRCPCRFEGG-----GGLKWIOE 24
Db 22 KPVSLSYRCPCRFESHVARANKHLKILNTPNCALQIVARLKNNGVCIDPKLKWIOE 81
QY 25 YLEKALN 31
Db 82 YLEKALN 88

RESULT 4
Q8UJ9 PRELIMINARY; PRT; 94 AA.
ID Q8UJ9
AC Q8UJ9;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Stromal-derived factor 1 precursor.
GN SDF-1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Braun M., Wunderlin M., Knoechel W., Gierschik P., Moepf B.;
RT "Xenopus laevis stromal-derived factor 1: conservation of structure
and function during vertebrate development.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ278857; CAC82196.1; -.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
FT SIGNAL.
FT CHAIN
FT CHAIN 22
SQ SEQUENCE 94 AA; 10701 MW; 8C8325D152F326E7 CRC64;

Query Match 60.0%; Score 105; DB 13; Length 94;
Best Local Similarity 35.8%; Pred. No. 9.4e-08;
Matches 24; Conservative 1; Mismatches 6; Indels 36; Gaps 1;

QY 1 KPVSLSYRCPCRFEGG-----GGLKWIOE 24
Db 22 KPVSLSYRCPCRFESHVARANKHLKILSTNSCSLQIVARLKNNGKICLDPKTKWIOE 81
QY 25 YLEKALN 31
Db 82 YLEKALN 88

RESULT 5
Q93YP8 PRELIMINARY; PRT; 507 AA.
ID Q93YP8
AC Q93YP8;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Cellulose synthase catalytic subunit (Ath-A).
GN ATAG39350.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Nguyen M., Karlin-Neumann G., Southwick A., Lam B., Miranda M.,
RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
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RA Ecker J., Theologis A., Davis R.W.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M.,
 RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
 RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
 RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
 RA Sakurai T., Satou M., Seki M., Shin P., Yamada K., Shinzaki K.,
 RA Ecker J., Theologis A., Davis R.W.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY059858; AAL24340.1; -
 DR EMBL; AY093308; AAM13307.1; -
 DR InterPro; IPR005150; Cellulose_synt.
 DR Pfam; PF03552; Cellulose_synt; 1.
 SQ SEQUENCE 507 AA; 56665 MW; D04313743E31DE61 CRC64;

Query Match 34.9%; Score 61; DB 10; Length 507;
 Best Local Similarity 43.5%; Pred. No. 1.6;
 Matches 10; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

OY 3 VSLSYRCPCRFFGGGGLKWIQEV 25
 :||| : ||||| :
 Db 256 IFLSRHCPIMYGCGGLKWLERF 278

RESULT 6
 ID 048947 PRELIMINARY; PRT; 1084 AA.
 AC 048947;
 DT 01-JUN-1998 (TReMBLrel. 06, Created)
 DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)
 DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
 DE Cellulose synthase catalytic subunit.
 GN H-A OR T22F8.250 OR AT4G39350.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=9811412; PubMed=9445479;
 RA Arioli T., Peng L., Betzner A.S., Burn J., Wittke W., Herth W.,
 RA Camilleri C., Hofte H., Plazinski J., Birch R., Cork A., Glover J.,
 RA Redmond J., Williams R.E.;
 RT "Molecular analysis of cellulose biosynthesis in Arabidopsis.";
 RL Science 279:717-720(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Bevan M., Zimmermann W., Grueneisen A., Wambutt R., Bancroft I.,
 RA Mewes H.W., Mayer K.F.X., Schueller C.;
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Zimmermann W., Grueneisen A., Wambutt R., Kalicki J., Woldmann P.,
 RA Smith A., Mewes H.W., Lemcke K., Mayer K.F.X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF027173; AAC39335.1; -
 DR EMBL; AL050351; CAB43650.1; -
 DR EMBL; AL161595; CAB80598.1; -
 DR InterPro; IPR005150; Cellulose_synt.
 DR InterPro; IPR001841; Znf_ring.
 DR Pfam; PF03552; Cellulose_synt; 1.

DR SMART; SM00184; RING; 1.
 DR PROSITE; PS50089; 2F_RING_2; 1.
 SQ SEQUENCE 1084 AA; 122068 MW; 2F9B22D168D734E0 CRC64;

Query Match 34.9%; Score 61; DB 10; Length 1084;
 Best Local Similarity 43.5%; Pred. No. 3.7;
 Matches 10; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

OY 3 VSLSYRCPCRFFGGGGLKWIQEV 25
 :||| : ||||| :
 Db 833 IFLSRHCPIMYGCGGLKWLERF 855

RESULT 7
 ID 09SJ22 PRELIMINARY; PRT; 1088 AA.
 AC 09SJ22;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
 DE Putative cellulose synthase catalytic subunit.
 GN AT2G21770.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=20083487; PubMed=10617197;
 RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
 RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
 RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
 RA Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
 RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
 RA Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
 RA Salzberg S.L., Fraser C.M., Venter J.C.;
 RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.";
 RL Nature 402:761-768(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RA Lin X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC007019; AAD20396.1; -
 DR InterPro; IPR005150; Cellulose_synt.
 DR InterPro; IPR001841; Znf_ring.
 DR Pfam; PF03552; Cellulose_synt; 1.
 DR SMART; SM00184; RING; 1.
 SQ SEQUENCE 1088 AA; 123446 MW; 06057111860DC9F CRC64;

Query Match 34.9%; Score 61; DB 10; Length 1088;
 Best Local Similarity 43.5%; Pred. No. 3.7;
 Matches 10; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

OY 3 VSLSYRCPCRFFGGGGLKWIQEV 25
 :||| : ||||| :
 Db 837 IFLSRHCPIMYGCGGLKWLERF 859

RESULT 8
 ID 093155 PRELIMINARY; PRT; 974 AA.
 AC 093155;
 DT 01-MAY-1997 (TReMBLrel. 03, Created)
 DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
 DE Cellulose synthase.
 GN CEL1A1.
 OS Gossypium hirsutum (Upland cotton).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
OX NCBI_TaxID=3635;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=Acacia SJ-2; TISSUE=Fiber;
RX MEDLINE=97057296; PubMed=8901635;
RA Pear J.R., Kawagoe Y., Schreckengost W.E., Delmer D.P., Stalker D.M.;
RT "Higher plants contain homologs of the bacterial cels genes encoding
the catalytic subunit of cellulose synthase."
RL Proc. Natl. Acad. Sci. U.S.A. 93:12637-12642(1996).
DR EMBL; U58283; AAB37766.1; -
DR InterPro; IPR005150; Cellulose_synt; 1.
DR Pfam; PF03552; Cellulose_synt; 1.
SQ SEQUENCE 974 AA; 109703 MW; 2656CA2D05D100A7 CRC64;

Query Match 34.6%; Score 60.5; DB 10; Length 974;
Best Local Similarity 54.5%; Pred. No. 3.9;
Matches 12; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

QY 3 VLSYRCPCRF-FGGGGLKWIQ 23
Db 721 IFLSRHCPWYGGGRLKWLQ 742

RESULT 9

Q8W1W0 PRELIMINARY; PRT; 974 AA.
AC Q8W1W0;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Cellulose synthase A4.
GN CESA4.
OS Gossypium hirsutum (Upland cotton).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
OX NCBI_TaxID=3635;
RN [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=21608363; PubMed=11743074;
RA Kim H.-J., Triplett B.A.;
RT "Cotton Fiber Growth in Planta and in Vitro. Models for Plant Cell
Elongation and Cell Wall Biogenesis."
RL Plant Physiol. 127:1361-1366(2001).
DR EMBL; AF413210; AAL37718.1; -
DR InterPro; IPR005150; Cellulose_synt.
DR Pfam; PF03552; Cellulose_synt; 1.
SQ SEQUENCE 974 AA; 109499 MW; F8AFB66ABA2B8071 CRC64;

Query Match 34.6%; Score 60.5; DB 10; Length 974;
Best Local Similarity 54.5%; Pred. No. 3.9;
Matches 12; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

QY 3 VLSYRCPCRF-FGGGGLKWIQ 23
Db 721 IFLSRHCPWYGGGRLKWLQ 742

RESULT 10

Q8L778 PRELIMINARY; PRT; 346 AA.
AC Q8L778;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Cellulose synthase catalytic subunit.
GN AT5G09870.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.

OX NCBI_TaxID=3702;
RN [1]
RN SEQUENCE FROM N.A.
RA Southwick A., Nguyen M., Tripp M., Palm C.J., Jones T., Wu T.,
RA Carninci P., Chen H., Cheuk R., Chan M.M., Chang C.H., Dale J.M.,
RA Deng J.M., Hayashizaki Y., Hsuan V.W., Lee J.M., Ishida J., Kamiya A.,
RA Kawai J., Kim C.J., Narusaka M., Quach H.L., Sakurai T., Satou M.,
RA Seki M., Shin P., Tang C.C., Toriumi M., Wallender E.K., Wong C.,
RA Wu H.C., Yamada K., Yu G., Yuan S., Shinozaki K., Ecker J.,
RA Theologis A., Davis R.W.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY136423; AAM97089.1; -
DR InterPro; IPR005150; Cellulose_synt.
DR Pfam; PF03552; Cellulose_synt; 1.
SQ SEQUENCE 346 AA; 38558 MW; 80799D6E46D57090 CRC64;

Query Match 33.1%; Score 58; DB 10; Length 346;
Best Local Similarity 47.6%; Pred. No. 3;
Matches 10; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 3 VLSYRCPCRF-FGGGGLKWIQ 23
Db 96 IFLSRHCPWYGGGRLKWLQ 116

RESULT 11

Q94J06 PRELIMINARY; PRT; 366 AA.
AC Q94J06;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE AT5G64740/MVP7_7.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RN SEQUENCE FROM N.A.
RP Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Shinn P.,
RA Banh J., Bowser L., Carninci P., Chung M.K., Goldsmith A.D.,
RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
RA Nguyen M., Palm C.J., Pham P.K., Quach H.L., Sakano H., Sakurai T.,
RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
RA Yu G., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
RT "Arabidopsis cDNA clones."
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RN SEQUENCE FROM N.A.
RP Cheuk R., Chen H., Kim C.J., Shinn P., Bowser L., Carninci P.,
RA Chan M.M., Chang C.H., Dale J.M., Deng J.M., Hayashizaki Y.,
RA Hsuan V.W., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,
RA Nguyen M., Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M.,
RA Southwick A., Tang C.C., Toriumi M., Wallender E.K., Wong C., Wu H.C.,
RA Yamada K., Yu G., Yuan S., Shinozaki K., Davis R.W., Theologis A.,
RA Ecker J.R.;
RT "Arabidopsis ORF clones."
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF375439; AAK53023.1; -
DR EMBL; AY143957; AAN28896.1; -
DR InterPro; IPR005150; Cellulose_synt.
DR Pfam; PF03552; Cellulose_synt; 1.
SQ SEQUENCE 366 AA; 40788 MW; A287A60060D3EE2B CRC64;

QY

Query Match 33.1%; Score 58; DB 10; Length 366;
Best Local Similarity 47.6%; Pred. No. 3.2;
Matches 10; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 3 VLSYRCPCRF-FGGGGLKWIQ 23


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Db 116 IFLSRHCPWYGYGGGLKMLE 136
RESULT 12
O9I168
ID O9I168 PRELIMINARY; PRT; 469 AA.
AC O9I168;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE Probable class III aminotransferase.
GN PA2413.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
DR EMBL; AE004668; AAG05801.1; -
DR HSSP; P16932; 2DKB.
DR InterPro; IPR005814; AminoTrans_3.
DR InterPro; IPR004637; Dat.
DR Pfam; PF00202; aminotran_3; 1.
DR TIGRFAMS; TIGR00709; dat; 1.
DR PROSITE; PS00600; AA_TRANSFER_CLASS_3; 1.
KW Transferase; Aminotransferase; Complete proteome.
SQ SEQUENCE 469 AA; 50215 MW; FAAB575E8A44EE8 CRC64;

Query Match 33.1%; Score 58; DB 16; Length 469;
Best Local Similarity 43.3%; Pred. No. 4.2;
Matches 13; Conservative 1; Mismatches 16; Indels 0; Gaps 0;

QY 2 PVSLSYRCPCRFEGGGLKWIQYLEKALN 31
Db 199 PYPDYRCPFGLGGEAGVKANLHYLENLIN 228

RESULT 13
O9FIB9
ID O9FIB9 PRELIMINARY; PRT; 1069 AA.
AC O9FIB9;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE Cellulose synthase catalytic subunit.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Columbia;
RX MEDLINE=99156233; PubMed=10048488;
RA Asamizu E., Sato S., Kaneko T., Nakamura Y., Kotani H., Miyajima N.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. VIII.
RT Sequence features of the regions of 1,081,958 bp covered by seventeen
RT physically assigned P1 and TAC clones.";
RL DNA Res. 5:379-391(1998).
DR EMBL; AB016893; BAB09408.1; -
DR InterPro; IPR005150; Cellulose_synt.
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DR InterPro; IPR001841; Znf_Ring.
DR Pfam; PF03552; Cellulose_synt; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS50089; ZF_RING_2; 1.
SQ SEQUENCE 1069 AA; 120861 MW; D03ED5C578DB3E7C CRC64;

Query Match 33.1%; Score 58; DB 10; Length 1069;
Best Local Similarity 47.6%; Pred. No. 9.9;
Matches 10; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 3 VSLSYRCPCRFEGGGLKWIQ 23
Db 819 IFLSRHCPWYGYGGGLKMLE 839

RESULT 14
O65338
ID O65338 PRELIMINARY; PRT; 1081 AA.
AC O65338;
DT 01-AUG-1998 (Tremblrel. 07, Created)
DT 01-AUG-1998 (Tremblrel. 07, Last sequence update)
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE Cellulose synthase (Fragment).
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Wu L., Joshi C.P., Chiang V.L.;
RT "Araxcela, a new member of the cellulose synthase gene family from
RT Arabidopsis (Accession No. AF062485) (PGR98-114).";
RL Plant Physiol. 117:1125-1125(1998).
DR EMBL; AF062485; AAC29067.1; -
DR InterPro; IPR005150; Cellulose_synt.
DR InterPro; IPR001841; znf_ring.
DR Pfam; PF03552; Cellulose_synt; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS50089; ZF_RING_2; 1.
FT NON_TER 1
SQ SEQUENCE 1081 AA; 122446 MW; DC59A35A1713FD9F CRC64;

Query Match 33.1%; Score 58; DB 10; Length 1081;
Best Local Similarity 47.6%; Pred. No. 10;
Matches 10; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 3 VSLSYRCPCRFEGGGLKWIQ 23
Db 831 IFLSRHCPWYGYGGGLKMLE 851

RESULT 15
O9FGF9
ID O9FGF9 PRELIMINARY; PRT; 1084 AA.
AC O9FGF9;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE Cellulose synthase catalytic subunit.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Columbia;
RA Kaneko T., Katoh T., Asamizu E., Sato S., Nakamura Y., Kotani H.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. XI.";
RT Submitted (APR-1999) to the EMBL/Genbank/DBJ databases.
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DR EMBL: AB025637; BAB10307.1; .
DR InterPro: IPR005150; Cellulose_synt.
DR InterPro: IPR001841; Znf_ring.
DR Pfam: PF03552; Cellulose_synt; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS50089; ZF_RING_2; 1.
SQ SEQUENCE 1084 AA; 122501 MW; 1520439A5053608C CRC64;

Query Match 33.1%; Score 58; DB 10; Length 1084;
Best Local Similarity 47.6%; Pred. NO. 10;
Matches 10; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 3 VSLSYRCPCRFEGGGLKWIQ 23
: || | : |||||:
DB 834 IFLSRHCPIMWYGGGLKMLE 854

Search completed: October 9, 2003, 09:20:47
Job time : 100 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 9, 2003, 09:17:46 ; Search time 29 Seconds
(without alignments)
45.229 Million cell updates/sec

Title: US-09-835-107A-11
Perfect score: 175
Sequence: 1 KPVSLSYRCPCRFFGGGGLKWIQYLEKALN 31

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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3: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	117	66.9	89	1	US-08-181-556-2	Sequence 2, Appli
2	117	66.9	89	1	US-08-323-084A-1	Sequence 1, Appli
3	117	66.9	89	1	US-08-674-008-1	Sequence 1, Appli
4	117	66.9	93	1	US-08-323-084A-5	Sequence 5, Appli
5	117	66.9	93	1	US-08-674-008-5	Sequence 5, Appli
6	117	66.9	93	1	US-09-312-283C-421	Sequence 421, App
7	117	66.9	166	4	US-09-646-028-5	Sequence 5, Appli
8	117	66.9	177	4	US-09-646-028-54	Sequence 54, Appli
9	117	66.9	326	3	US-08-808-720-3	Sequence 3, Appli
10	117	66.9	328	3	US-08-808-720-1	Sequence 1, Appli
11	117	66.9	339	4	US-09-646-028-55	Sequence 55, Appli
12	117	66.9	339	4	US-09-646-028-55	Sequence 8, Appli
13	61	34.9	1084	4	US-09-221-013A-8	Sequence 6, Appli
14	60.5	34.6	974	3	US-08-960-048-6	Sequence 6, Appli
15	58	33.1	535	4	US-09-838-586-6	Sequence 25662, A
16	50	28.6	588	3	US-09-252-991A-25662	Sequence 16, Appli
17	50	28.6	588	3	PCT-US93-00869-16	Sequence 16, Appli
18	50	28.6	685	3	US-08-960-048-7	Sequence 7, Appli
19	50	28.6	685	3	US-09-838-586-7	Sequence 7, Appli
20	49.5	28.3	504	4	US-09-252-991A-32272	Sequence 32272, A
21	49	28.0	416	1	US-08-117-083-61	Sequence 61, Appli
22	49	28.0	488	3	US-08-311-731A-29	Sequence 29, Appli
23	48	27.4	78	3	US-09-188-930-158	Sequence 158, App
24	48	27.4	78	3	US-09-188-930-285	Sequence 285, App
25	48	27.4	78	4	US-09-312-283C-158	Sequence 158, App
26	48	27.4	78	4	US-09-312-283C-285	Sequence 285, App
27	48	27.4	125	3	US-08-722-126A-7	Sequence 7, Appli

28	48	27.4	125	5	PCT-US95-04258-7	Sequence 7, Appli
29	48	27.4	287	1	US-08-365-103B-4	Sequence 4, Appli
30	48	27.4	300	1	US-08-365-103B-6	Sequence 6, Appli
31	48	27.4	327	1	US-08-365-103B-2	Sequence 2, Appli
32	48	27.4	580	4	US-09-252-991A-30180	Sequence 30180, A
33	47.5	27.1	305	4	US-09-252-991A-26204	Sequence 26204, A
34	46	26.3	186	1	US-08-089-458B-6	Sequence 6, Appli
35	46	26.3	455	6	5168051-11	Patent No. 5168051
36	46	26.3	927	4	US-09-252-991A-20340	Sequence 20340, A
37	45	25.7	173	4	US-09-252-991A-32359	Sequence 32359, A
38	45	25.7	252	4	US-09-198-452A-1215	Sequence 1215, Ap
39	45	25.7	292	2	US-08-701-191A-40	Sequence 40, Appli
40	45	25.7	514	4	US-09-266-965-114	Sequence 114, App
41	45	25.7	581	1	US-08-446-038B-17	Sequence 17, Appli
42	45	25.7	581	1	US-08-446-010B-17	Sequence 17, Appli
43	45	25.7	581	2	US-08-805-445-17	Sequence 17, Appli
44	45	25.7	581	2	US-08-064-067D-17	Sequence 17, Appli
45	45	25.7	581	2	US-09-066-208-17	Sequence 17, Appli

ALIGNMENTS

RESULT 1
US-08-181-556-2
Sequence 2, Application US/08181556
Patent No. 5525486
GENERAL INFORMATION:
APPLICANT: HONJO, Tasuku
APPLICANT: TASHIRO, Kei
TITLE OF INVENTION: PROCESS FOR CONSTRUCTING CDNA LIBRARY,
TITLE OF INVENTION: AND NOVEL POLYPEPTIDE AND DNA CODING FOR THE SAME
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: STEVENS, DAVIS, MILLER & MOSHER
STREET: 515 No. 5525486th Washington Street (P.O. Box 1427)
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22313
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/181,556
FILING DATE: 14-JAN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-22098
FILING DATE: 14-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: POULOS III, James A.
REGISTRATION NUMBER: 31714
REFERENCE/DOCKET NUMBER: TTP/29088
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 549-7200
TELEFAX: (703) 528-5313
TELEX: 89-2746
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 89 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-181-556-2

Query Match 66.9%; Score 117; DB 1; Length 89;
Best Local Similarity 40.3%; Pred. No. 6.6e-09;
Matches 27; Conservative 0; Mismatches 4; Indels 36; Gaps 1;

QY 1 KPVSLSYRCPCRFEGG-----GGLKWIQE 24
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DB 22 KPVSLSYRCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNROYCIDPKLKWIOE 81
QY 25 YLEKALN 31
|||||
DB 82 YLEKALN 88

RESULT 2

US-08-323-084A-1
; Sequence 1, Application US/08323084A
; Patent No. 5563048
; GENERAL INFORMATION:
; APPLICANT: HONJO, TASUKU
; APPLICANT: SHIROZU, MICHIO
; APPLICANT: TADA, HIDEAKI
; TITLE OF INVENTION: No. 5563048e1 Polypeptides and DNAs encoding them
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20037-3202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/323,084A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 280505/1993
; FILING DATE: 14-OCT-1993
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)293-7060
; TELEFAX: (202)293-7860
; TELEX: 6491103
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 89 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-323-084A-1

Query Match 66.9%; Score 117; DB 1; Length 89;
Best Local Similarity 40.3%; Pred. No. 6.6e-09;
Matches 27; Conservative 0; Mismatches 4; Indels 36; Gaps 1;

QY 1 KPVSLSYRCPCRFEGG-----GGLKWIQE 24
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DB 22 KPVSLSYRCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNROYCIDPKLKWIOE 81

QY 25 YLEKALN 31
|||||
DB 82 YLEKALN 88

RESULT 3

US-08-674-008-1
; Sequence 1, Application US/08674008
; Patent No. 5756084
; GENERAL INFORMATION:
; APPLICANT: HONJO, Tasuku
; APPLICANT: SHIROZU, Michio
; APPLICANT: TADA, Hideaki
; TITLE OF INVENTION: HUMAN STROMAL DERIVED
; TITLE OF INVENTION: FACTOR 1, AND 1 (As Amended)

NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20037-3202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/674,008
; FILING DATE: 1-JUL-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/323,084
; FILING DATE: 14-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 280505/1993
; FILING DATE: 14-OCT-1993
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)293-7060
; TELEFAX: (202)293-7860
; TELEX: 6491103
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 89 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-674-008-1

Query Match 66.9%; Score 117; DB 1; Length 89;
Best Local Similarity 40.3%; Pred. No. 6.6e-09;
Matches 27; Conservative 0; Mismatches 4; Indels 36; Gaps 1;

QY 1 KPVSLSYRCPCRFEGG-----GGLKWIQE 24
|||||
DB 22 KPVSLSYRCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNROYCIDPKLKWIOE 81

QY 25 YLEKALN 31
|||||
DB 82 YLEKALN 88

RESULT 4

US-08-323-084A-5
; Sequence 5, Application US/08323084A
; Patent No. 5563048
; GENERAL INFORMATION:
; APPLICANT: HONJO, TASUKU
; APPLICANT: SHIROZU, MICHIO
; APPLICANT: TADA, HIDEAKI
; TITLE OF INVENTION: No. 5563048e1 Polypeptides and DNAs encoding them
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20037-3202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/323,084A
; FILING DATE:

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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 280505/1993
FILING DATE: 14-OCT-1993
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
TELEFAX: (202)293-7860
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 93 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-323-084A-5

Query Match      66.9%; Score 117; DB 1; Length 93;
Best Local Similarity 40.3%; Pred. No. 6.9e-09;
Matches 27; Conservative 0; Mismatches 4; Indels 36; Gaps 1;

QY      1 KPVSLSYRCPCRFFGG-----GGLKWIQE 24
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Db      22 KPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 81

QY      25 YLEKALN 31
      |||||
Db      82 YLEKALN 88

RESULT 5
US-08-674-008-5
Sequence 5, Application US/08674008
Patent No. 5756084
GENERAL INFORMATION:
APPLICANT: HONJO, Tasuku
APPLICANT: SHIROZU, Michio
APPLICANT: TADA, Hideaki
TITLE OF INVENTION: HUMAN STROMAL DERIVED
TITLE OF INVENTION: FACTOR 1 AND 1 (As Amended)
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20037-3202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/674,008
FILING DATE: 1-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/323,084
FILING DATE: 14-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 280505/1993
FILING DATE: 14-OCT-1993
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
TELEFAX: (202)293-7860
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 93 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-674-008-5
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Query Match      66.9%; Score 117; DB 1; Length 93;
Best Local Similarity 40.3%; Pred. No. 6.9e-09;
Matches 27; Conservative 0; Mismatches 4; Indels 36; Gaps 1;

QY      1 KPVSLSYRCPCRFFGG-----GGLKWIQE 24
      |||||
Db      22 KPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 81

QY      25 YLEKALN 31
      |||||
Db      82 YLEKALN 88

RESULT 6
US-09-312-283C-421
Sequence 421, Application US/09312283C
Patent No. 6573095
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James G.
APPLICANT: Kumble, Krishanand D.
TITLE OF INVENTION: Compositions Isolated from Skin Cells
TITLE OF INVENTION: and Methods for their use
FILE REFERENCE: 11000.1011c2
CURRENT APPLICATION NUMBER: US/09/312,283C
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 425
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 421
LENGTH: 93
TYPE: PRT
ORGANISM: Mouse
US-09-312-283C-421

Query Match      66.9%; Score 117; DB 4; Length 93;
Best Local Similarity 40.3%; Pred. No. 6.9e-09;
Matches 27; Conservative 0; Mismatches 4; Indels 36; Gaps 1;

QY      1 KPVSLSYRCPCRFFGG-----GGLKWIQE 24
      |||||
Db      22 KPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 81

QY      25 YLEKALN 31
      |||||
Db      82 YLEKALN 88

RESULT 7
US-09-646-028-5
Sequence 5, Application US/09646028
Patent No. 6562347
GENERAL INFORMATION:
APPLICANT: Kwak, Larry
APPLICANT: Biragyn, Arya
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
TITLE OF INVENTION: CHEMOKINE-TUMOR ANTIGEN FUSION PROTEINS AS CANCER VACCINES
FILE REFERENCE: 14014.0316/P
CURRENT APPLICATION NUMBER: US/09/646,028
CURRENT FILING DATE: 2000-09-12
PRIOR APPLICATION NUMBER: 60/077,745
PRIOR FILING DATE: 1998-03-12
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 5
LENGTH: 166
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct
US-09-646-028-5
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US-09-646-028-5

Query Match 66.9%; Score 117; DB 4; Length 166;
Best Local Similarity 40.3%; Pred. No. 1.2e-08;
Matches 27; Conservative 0; Mismatches 4; Indels 36; Gaps 1;

QY 1 KPVSLSYRCPRCRFFGG-----GGLKWIQE 24
Db 22 KPVSLSYRCPRCRFFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 81
QY 25 YLEKALN 31
Db 82 YLEKALN 88

RESULT 8

US-09-646-028-54

; Sequence 54, Application US/09646028
; Patent No. 6562347

GENERAL INFORMATION:

APPLICANT: Kwak, Larry

APPLICANT: Biragyn, Arya

TITLE OF INVENTION: METHODS AND COMPOSITIONS OF

TITLE OF INVENTION: CHEMOKINE-TUMOR ANTIGEN FUSION PROTEINS AS CANCER VACCINES

FILE REFERENCE: 14014.0316/P

CURRENT APPLICATION NUMBER: US/09/646,028

CURRENT FILING DATE: 2000-09-12

PRIOR APPLICATION NUMBER: 60/077,745

PRIOR FILING DATE: 1998-03-12

NUMBER OF SEQ ID NOS: 57

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 54

LENGTH: 177

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct

US-09-646-028-54

Query Match 66.9%; Score 117; DB 4; Length 177;
Best Local Similarity 40.3%; Pred. No. 1.3e-08;
Matches 27; Conservative 0; Mismatches 4; Indels 36; Gaps 1;

QY 1 KPVSLSYRCPRCRFFGG-----GGLKWIQE 24
Db 4 KPVSLSYRCPRCRFFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 63
QY 25 YLEKALN 31
Db 64 YLEKALN 70

RESULT 9

US-08-808-720-3

; Sequence 3, Application US/08808720
; Patent No. 6100387

GENERAL INFORMATION:

APPLICANT: Herrmann, Steve

APPLICANT: Swandberg, Stephen

TITLE OF INVENTION: CHIMERIC POLYPEPTIDES CONTAINING

TITLE OF INVENTION: CHEMOKINE DOMAINS

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genetics Institute, Inc.

STREET: 87 Cambridgepark

CITY: Cambridge

STATE: MA

COUNTRY: USA

ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/808,720

FILING DATE:

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Sprunger, Suzanne

REGISTRATION NUMBER: P-41,323

REFERENCE/DOCKET NUMBER: G15291

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 498-8284

TELEFAX: (617) 876-5851

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 326 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-808-720-3

Query Match 66.9%; Score 117; DB 3; Length 326;
Best Local Similarity 40.3%; Pred. No. 2.5e-08;
Matches 27; Conservative 0; Mismatches 4; Indels 36; Gaps 1;

QY 1 KPVSLSYRCPRCRFFGG-----GGLKWIQE 24
Db 20 KPVSLSYRCPRCRFFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 79
QY 25 YLEKALN 31
Db 80 YLEKALN 86

RESULT 10

US-08-808-720-1

; Sequence 1, Application US/08808720
; Patent No. 6100387

GENERAL INFORMATION:

APPLICANT: Herrmann, Steve

APPLICANT: Swandberg, Stephen

TITLE OF INVENTION: CHIMERIC POLYPEPTIDES CONTAINING

TITLE OF INVENTION: CHEMOKINE DOMAINS

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genetics Institute, Inc.

STREET: 87 Cambridgepark

CITY: Cambridge

STATE: MA

COUNTRY: USA

ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/808,720

FILING DATE:

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Sprunger, Suzanne

REGISTRATION NUMBER: P-41,323

REFERENCE/DOCKET NUMBER: G15291

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 498-8284

TELEFAX: (617) 876-5851

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 328 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-808-720-1

Query Match 66.9%; Score 117; DB 3; Length 328;
Best Local Similarity 40.3%; Pred. No. 2.5e-08;
Matches 27; Conservative 0; Mismatches 4; Indels 36; Gaps 1;

QY 1 KPVSLSYRCPRCRFFGG-----GGLKWIQE 24
DB 22 KPVSLSYRCPRCRFFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIQE 81
QY 25 YLEKALN 31
DB 82 YLEKALN 88

RESULT 11

US-09-646-028-55
Sequence 55, Application US/09646028
Patent No. 6562347

GENERAL INFORMATION:

APPLICANT: Biragyn, Larry

TITLE OF INVENTION: METHODS AND COMPOSITIONS OF

TITLE OF INVENTION: CHEMOKINE-TUMOR ANTIGEN FUSION PROTEINS AS CANCER VACCINES

FILE REFERENCE: 14014.0316/P

CURRENT APPLICATION NUMBER: US/09/646,028

PRIOR FILING DATE: 2000-09-12

PRIOR APPLICATION NUMBER: 60/077,745

NUMBER OF SEQ ID NOS: 57

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 55

LENGTH: 339

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct

US-09-646-028-55

Query Match 66.9%; Score 117; DB 4; Length 339;
Best Local Similarity 40.3%; Pred. No. 2.6e-08;
Matches 27; Conservative 0; Mismatches 4; Indels 36; Gaps 1;

QY 1 KPVSLSYRCPRCRFFGG-----GGLKWIQE 24
DB 4 KPVSLSYRCPRCRFFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIQE 63

QY 25 YLEKALN 31
DB 64 YLEKALN 70

RESULT 12

US-09-221-013A-8
Sequence 8, Application US/09221013A
Patent No. 6495740

GENERAL INFORMATION:

APPLICANT: Arioli, Antonio

APPLICANT: Williamson, Richard E.

APPLICANT: Belzner, Andreas S.

APPLICANT: Peng, Liangcai

TITLE OF INVENTION: Manipulation of cellulose and/or Beta-1,4-glucan

FILE REFERENCE: 96-98

CURRENT APPLICATION NUMBER: US/09/221,013A

PRIOR FILING DATE: 1998-12-23

PRIOR APPLICATION NUMBER: PCT/AU97/00402

PRIOR FILING DATE: 1997-06-24

PRIOR APPLICATION NUMBER: AU P00699

PRIOR FILING DATE: 1996-06-27

NUMBER OF SEQ ID NOS: 37

SOFTWARE: Patentln Ver. 2.0

SEQ ID NO 8

LENGTH: 1084

TYPE: PRT

ORGANISM: Arabidopsis thaliana

US-09-221-013A-8

Query Match 34.9%; Score 61; DB 4; Length 1084;
Best Local Similarity 43.5%; Pred. No. 3.6;
Matches 10; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 3 VSLSYRCPRCRFFGGGGLKWIQEY 25
DB 833 IFLSRHCPIMWYGGGGLKWLERF 855

RESULT 13

US-08-960-048-6
Sequence 6, Application US/08960048C
Patent No. 6271443

GENERAL INFORMATION:

APPLICANT: Stalker, D. et al.

TITLE OF INVENTION: Plant Cellulose Synthase and Promoter

FILE REFERENCE: 15621/01/US

CURRENT APPLICATION NUMBER: US/08/960,048C

PRIOR FILING DATE: 1997-10-29

PRIOR APPLICATION NUMBER: 60/029,987

NUMBER OF SEQ ID NOS: 12

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 6

LENGTH: 974

TYPE: PRT

ORGANISM: Gossypium hirsutum

US-08-960-048-6

Query Match 34.6%; Score 60.5; DB 3; Length 974;
Best Local Similarity 54.5%; Pred. No. 3.8;
Matches 12; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

QY 3 VSLSYRCPRCRFFGGGGLKWIQ 23
DB 721 IFLSRHCPIMWYGFGGGLKWIQ 742

RESULT 14

US-09-838-586-6
Sequence 6, Application US/09838586
Patent No. 6576818

GENERAL INFORMATION:

APPLICANT: Stalker, D. et al.

TITLE OF INVENTION: Plant Cellulose Synthase and Promoter

FILE REFERENCE: 15621/02/US

CURRENT APPLICATION NUMBER: US/09/838,586

PRIOR FILING DATE: 2001-04-18

PRIOR APPLICATION NUMBER: 60/029,987

PRIOR FILING DATE: 1996-10-29

PRIOR APPLICATION NUMBER: 08/960,048

PRIOR FILING DATE: 1997-10-29

NUMBER OF SEQ ID NOS: 12

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 6

LENGTH: 974

TYPE: PRT

ORGANISM: Gossypium hirsutum

US-09-838-586-6

Query Match 34.6%; Score 60.5; DB 4; Length 974;
Best Local Similarity 54.5%; Pred. No. 3.8;
Matches 12; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

QY 3 VSLSYRCPRCRFFGGGGLKWIQ 23

Db 721 IFLSRHCPIMYGGGRLKWLQ 742

RESULT 15

US-09-252-991A-25662

; Sequence 25662, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 25662

; LENGTH: 535

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-25662

Query Match 33.1%; Score 58; DB 4; Length 535;

Best Local Similarity 43.3%; Pred. No. 4.6;

Matches 13; Conservative 1; Mismatches 16; Indels 0; Gaps 0;

QY 2 PVSLSYRCPCRFEGGGLKWIQYLEKALN 31

Db 265 PYPYDYRCPFGLGEGAGVKANLHYLENLN 294

Search completed: October 9, 2003, 09:22:07
Job time : 30 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 9, 2003, 09:18:21 ; Search time 375 Seconds
(Without alignments)
13.320 Million cell updates/sec

Title: US-09-835-107A-11
Perfect score: 175
Sequence: 1 KPVSLSYRCPRCRFFGGGLKWIQYLEKALN 31

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 600653 seqs, 161128416 residues

Total number of hits satisfying chosen parameters: 600653

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications_AA:*

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- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
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- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	175	100.0	31	10	US-09-835-107-13
2	175	100.0	31	10	US-09-835-107-15
3	175	100.0	31	10	US-09-835-107-20
4	175	100.0	31	10	US-09-835-107-21
5	175	100.0	31	10	US-09-835-107-22
6	175	100.0	31	10	US-09-835-107-23
7	175	100.0	31	10	US-09-835-107-26
8	175	100.0	31	10	US-09-835-107-27
9	175	100.0	31	12	US-10-086-177A-13
10	175	100.0	31	12	US-10-086-177A-15
11	175	100.0	31	12	US-10-086-177A-20
12	175	100.0	31	12	US-10-086-177A-21
13	175	100.0	31	12	US-10-086-177A-22
14	175	100.0	31	12	US-10-086-177A-23
15	175	100.0	31	12	US-10-086-177A-26

16	175	100.0	31	12	US-10-086-177A-27	Sequence 27, Appl
17	172	98.3	31	10	US-09-835-107-24	Sequence 24, Appl
18	172	98.3	31	10	US-09-835-107-25	Sequence 25, Appl
19	172	98.3	31	12	US-10-086-177A-24	Sequence 24, Appl
20	172	98.3	31	12	US-10-086-177A-25	Sequence 25, Appl
21	166	94.9	31	10	US-09-852-424-74	Sequence 74, Appl
22	166	94.9	31	10	US-09-852-424-122	Sequence 122, App
23	166	94.9	31	10	US-09-852-424-124	Sequence 124, App
24	166	94.9	31	10	US-09-852-424-133	Sequence 133, App
25	166	94.9	31	10	US-09-852-424-134	Sequence 134, App
26	166	94.9	31	10	US-09-852-424-135	Sequence 135, App
27	163.5	93.4	34	10	US-09-835-107-17	Sequence 17, Appl
28	163.5	93.4	34	10	US-09-835-107-19	Sequence 19, Appl
29	163.5	93.4	34	12	US-10-086-177A-17	Sequence 17, Appl
30	163.5	93.4	34	12	US-10-086-177A-19	Sequence 19, Appl
31	162	92.6	31	10	US-09-852-424-95	Sequence 95, Appl
32	161	92.0	31	10	US-09-852-424-79	Sequence 79, Appl
33	161	92.0	31	10	US-09-852-424-94	Sequence 94, Appl
34	160	91.4	31	10	US-09-852-424-97	Sequence 97, Appl
35	159	90.9	31	10	US-09-852-424-81	Sequence 81, Appl
36	159	90.9	31	10	US-09-852-424-78	Sequence 78, Appl
37	158.5	90.6	30	10	US-09-835-107-12	Sequence 12, Appl
38	158.5	90.6	30	10	US-09-835-107-14	Sequence 14, Appl
39	158.5	90.6	30	12	US-10-086-177A-12	Sequence 12, Appl
40	158.5	90.6	30	12	US-10-086-177A-14	Sequence 14, Appl
41	158	90.3	31	10	US-09-852-424-96	Sequence 96, Appl
42	156	89.1	31	10	US-09-852-424-80	Sequence 80, Appl
43	156	89.1	33	10	US-09-835-107-16	Sequence 16, Appl
44	156	89.1	33	10	US-09-835-107-18	Sequence 18, Appl
45	156	89.1	33	12	US-10-086-177A-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-09-835-107-13
US-09-835-107-13, Application US/09835107
Patent No. US20020165123A1
GENERAL INFORMATION:
APPLICANT: Tudan, Christopher R.
APPLICANT: Merzouk, Ahmed
APPLICANT: Arab, Lakhdar
APPLICANT: Saxena, Geeta
APPLICANT: Eaves, Connie J.
APPLICANT: Cashman, Johanne
APPLICANT: Clark-Lewis
APPLICANT: Salari, Hassan
TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS
FILE REFERENCE: SMAR012
CURRENT APPLICATION NUMBER: US/09/835,107
CURRENT FILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: CA 2,305,036
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: US 60/232,425
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: CA 2,335,109
PRIOR FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 13
LENGTH: 31
TYPE: PRT
ORGANISM: Artificial Sequence
NAME/KEY: DOMAIN
LOCATION: (16)..(19)
OTHER INFORMATION: spacer monomers (such as the illustrated glycine
OTHER INFORMATION: G's) may be used in variable numbers, such as 2, 3
OTHER INFORMATION: or 4 glycines.
OTHER INFORMATION: Synthesised in Laboratory:
OTHER INFORMATION: SDF-1(1-14)-(G)4-SDF-1(55-67) acid: or CTCE0013
US-09-835-107-13

Query Match 100.0%; Score 175; DB 10; Length 31;
Best Local Similarity 100.0%; Pred. No. 4.9e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVSLSYRCPCRFFGGGLKWIQIYLEKALN 31
|||||
Db 1 KPVSLSYRCPCRFFGGGLKWIQIYLEKALN 31

RESULT 2

US-09-835-107-15

; Sequence 15, Application US/09835107
; Patent No. US20020165123A1
; GENERAL INFORMATION:

; APPLICANT: Tudan, Christopher R.

; APPLICANT: Merzouk, Ahmed

; APPLICANT: Arab, Lakhdar

; APPLICANT: Saxena, Geeta

; APPLICANT: Eaves, Connie J.

; APPLICANT: Cashman, Johanne

; APPLICANT: Clark-Lewis

; APPLICANT: Salari, Hassan

; TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS

; FILE REFERENCE: SMAR012

; CURRENT APPLICATION NUMBER: US/09/835,107

; CURRENT FILING DATE: 2001-08-20

; PRIOR APPLICATION NUMBER: CA 2,305,036

; PRIOR FILING DATE: 2000-04-12

; PRIOR APPLICATION NUMBER: US 60/232,425

; PRIOR FILING DATE: 2000-09-14

; PRIOR APPLICATION NUMBER: CA 2,335,109

; PRIOR FILING DATE: 2001-02-23

; NUMBER OF SEQ ID NOS: 34

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 15

; LENGTH: 31

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; NAME/KEY: DOMAIN

; LOCATION: (15)..(18)

; OTHER INFORMATION: spacer monomers (such as the illustrated glycine

; OTHER INFORMATION: G's) may be used in variable numbers, such as 2, 3

; OTHER INFORMATION: or 4 glycines.

; OTHER INFORMATION: Synthesised in Laboratory:

; OTHER INFORMATION: SDF-1(1-14)-(G)4-SDF-1(55-67) amide: or CTCE0017

; NAME/KEY: MOD_RES

; LOCATION: (31)

; OTHER INFORMATION: AMIDATION

; US-09-835-107-15

; Query Match

100.0%; Score 175; DB 10; Length 31;
Best Local Similarity 100.0%; Pred. No. 4.9e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVSLSYRCPCRFFGGGLKWIQIYLEKALN 31
|||||
Db 1 KPVSLSYRCPCRFFGGGLKWIQIYLEKALN 31

RESULT 3

US-09-835-107-20

; Sequence 20, Application US/09835107
; Patent No. US20020165123A1
; GENERAL INFORMATION:

; APPLICANT: Tudan, Christopher R.

; APPLICANT: Merzouk, Ahmed

; APPLICANT: Arab, Lakhdar

; APPLICANT: Saxena, Geeta

; APPLICANT: Eaves, Connie J.

; APPLICANT: Cashman, Johanne

; APPLICANT: Clark-Lewis

; APPLICANT: Salari, Hassan

; TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS

; FILE REFERENCE: SMAR012

; CURRENT APPLICATION NUMBER: US/09/835,107

; CURRENT FILING DATE: 2001-08-20

; PRIOR APPLICATION NUMBER: CA 2,305,036

; PRIOR FILING DATE: 2000-04-12

; PRIOR APPLICATION NUMBER: US 60/232,425

; PRIOR FILING DATE: 2000-09-14

; PRIOR APPLICATION NUMBER: CA 2,335,109

; PRIOR FILING DATE: 2001-02-23

; NUMBER OF SEQ ID NOS: 34

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 20

; LENGTH: 31

; TYPE: PRT

; ORGANISM: Artificial Sequence

; NAME/KEY: DOMAIN

; LOCATION: (15)..(18)

; OTHER INFORMATION: spacer monomers (such as the illustrated glycine

; OTHER INFORMATION: G's) may be used in variable numbers, such as 2, 3

; OTHER INFORMATION: or 4 glycines.

; NAME/KEY: DOMAIN

; LOCATION: (24)..(28)

; OTHER INFORMATION: cyclized, for example glutamate (E) and lysine (K)

; OTHER INFORMATION: residues may be joined by side chain cyclization

; OTHER INFORMATION: using a lactam formation procedure.

; OTHER INFORMATION: Synthesised in Laboratory:

; OTHER INFORMATION: SDF-1(1-14)-(G)4-SDF(55-67)-E24/K28-cyclic acid

; US-09-835-107-20

Query Match 100.0%; Score 175; DB 10; Length 31;
Best Local Similarity 100.0%; Pred. No. 4.9e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVSLSYRCPCRFFGGGLKWIQIYLEKALN 31
|||||
Db 1 KPVSLSYRCPCRFFGGGLKWIQIYLEKALN 31

RESULT 4

US-09-835-107-21

; Sequence 21, Application US/09835107
; Patent No. US20020165123A1
; GENERAL INFORMATION:

; APPLICANT: Tudan, Christopher R.

; APPLICANT: Merzouk, Ahmed

; APPLICANT: Arab, Lakhdar

; APPLICANT: Saxena, Geeta

; APPLICANT: Eaves, Connie J.

; APPLICANT: Cashman, Johanne

; APPLICANT: Clark-Lewis

; APPLICANT: Salari, Hassan

; TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS

; FILE REFERENCE: SMAR012

; CURRENT APPLICATION NUMBER: US/09/835,107

; CURRENT FILING DATE: 2001-08-20

; PRIOR APPLICATION NUMBER: CA 2,305,036

; PRIOR FILING DATE: 2000-04-12

; PRIOR APPLICATION NUMBER: US 60/232,425

; PRIOR FILING DATE: 2000-09-14

; PRIOR APPLICATION NUMBER: CA 2,335,109

; PRIOR FILING DATE: 2001-02-23

; NUMBER OF SEQ ID NOS: 34

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 21

; LENGTH: 31

; TYPE: PRT

; ORGANISM: Artificial Sequence

; NAME/KEY: DOMAIN

; LOCATION: (15)..(18)


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OTHER INFORMATION: spacer monomers (such as the illustrated glycine
OTHER INFORMATION: G's) may be used in variable numbers, such as 2, 3
OTHER INFORMATION: or 4 glycines.
NAME/KEY: DOMAIN
LOCATION: (20)..(24)
OTHER INFORMATION: Cyclized, for example glutamate (E) and lysine (K)
OTHER INFORMATION: residues may be joined by side chain cyclization
OTHER INFORMATION: using a lactam formation.
OTHER INFORMATION: Synthesised in Laboratory:
OTHER INFORMATION: SDF-1(1-14)-(G)4-SDF-1(55-67)-K20/E24-cyclic acid
US-09-835-107-21
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```
Query Match      100.0%; Score 175; DB 10; Length 31;
Best Local Similarity 100.0%; Pred. No. 4.9e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 KPVSLSYRCPCRFPGGGGLKWIQIYLEKALN 31
Db      1 KPVSLSYRCPCRFPGGGGLKWIQIYLEKALN 31
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RESULT 5
US-09-835-107-22
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Sequence 22, Application US/09835107
Patent No. US20020165123A1
GENERAL INFORMATION:
APPLICANT: Tudan, Christopher R.
APPLICANT: Merzouk, Ahmed
APPLICANT: Arab, Lakhdar
APPLICANT: Saxena, Geeta
APPLICANT: Eaves, Connie J.
APPLICANT: Cashman, Johanne
APPLICANT: Clark-Lewis
APPLICANT: Salari, Hassan
TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS
FILE REFERENCE: SMAR012
CURRENT APPLICATION NUMBER: US/09/835,107
CURRENT FILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: CA 2,305,036
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: US 60/232,425
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: CA 2,335,109
PRIOR FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 22
LENGTH: 31
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (15)..(18)
OTHER INFORMATION: spacer monomers (such as the illustrated glycine
OTHER INFORMATION: G's) may be used in variable numbers, such as 2, 3
OTHER INFORMATION: or 4 glycines.
NAME/KEY: DOMAIN
LOCATION: (24)..(28)
OTHER INFORMATION: Cyclized, for example (E) and lysine (K) residues
OTHER INFORMATION: may be joined by side chain cyclization using a
OTHER INFORMATION: lactam formation procedure.
OTHER INFORMATION: Synthesised in Laboratory:
OTHER INFORMATION: SDF-1(1-14)-(G)4-SDF-1(55-67)-E24/K28-cyclic
OTHER INFORMATION: amide: or CTCE0022
NAME/KEY: MOD_RES
LOCATION: (31)
OTHER INFORMATION: AMIDATION
US-09-835-107-22
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Query Match      100.0%; Score 175; DB 10; Length 31;
Best Local Similarity 100.0%; Pred. No. 4.9e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 KPVSLSYRCPCRFPGGGGLKWIQIYLEKALN 31
Db      1 KPVSLSYRCPCRFPGGGGLKWIQIYLEKALN 31
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RESULT 6
US-09-835-107-23
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Sequence 23, Application US/09835107
Patent No. US20020165123A1
GENERAL INFORMATION:
APPLICANT: Tudan, Christopher R.
APPLICANT: Merzouk, Ahmed
APPLICANT: Arab, Lakhdar
APPLICANT: Saxena, Geeta
APPLICANT: Eaves, Connie J.
APPLICANT: Cashman, Johanne
APPLICANT: Clark-Lewis
APPLICANT: Salari, Hassan
TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS
FILE REFERENCE: SMAR012
CURRENT APPLICATION NUMBER: US/09/835,107
CURRENT FILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: CA 2,305,036
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: US 60/232,425
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: CA 2,335,109
PRIOR FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 23
LENGTH: 31
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (15)..(18)
OTHER INFORMATION: spacer monomers (such as the illustrated glycine
OTHER INFORMATION: G's) may be used in variable numbers, such as 2, 3
OTHER INFORMATION: or 4 glycines.
NAME/KEY: DOMAIN
LOCATION: (20)..(24)
OTHER INFORMATION: Cyclized, for example glutamate (E) and lysine
OTHER INFORMATION: (K) residues may be joined by side chain
OTHER INFORMATION: cyclization using a lactam formation procedure.
OTHER INFORMATION: Synthesised in Laboratory:
OTHER INFORMATION: SDF-1(1-14)-(G)4-SDF-1(55-67)-K20/E24-cyclic
OTHER INFORMATION: amide: or CTCE0021
NAME/KEY: MOD_RES
LOCATION: (31)
OTHER INFORMATION: AMIDATION
US-09-835-107-23
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```
Query Match      100.0%; Score 175; DB 10; Length 31;
Best Local Similarity 100.0%; Pred. No. 4.9e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KPVSLSYRCPCRFPGGGGLKWIQIYLEKALN 31
Db      1 KPVSLSYRCPCRFPGGGGLKWIQIYLEKALN 31
```

```
RESULT 7
US-09-835-107-26
```

```
Sequence 26, Application US/09835107
Patent No. US20020165123A1
GENERAL INFORMATION:
APPLICANT: Tudan, Christopher R.
APPLICANT: Merzouk, Ahmed
APPLICANT: Arab, Lakhdar
APPLICANT: Saxena, Geeta
APPLICANT: Eaves, Connie J.
APPLICANT: Cashman, Johanne
```

```
; APPLICANT: Clark-Lewis
; APPLICANT: Salari, Hassan
; TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS
; FILE REFERENCE: SMAR012
; CURRENT APPLICATION NUMBER: US/09/835,107
; CURRENT FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: CA 2,305,036
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/232,425
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: CA 2,335,109
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (15)..(18)
; OTHER INFORMATION: spacer monomers (such as the illustrated glycine
; OTHER INFORMATION: G's) may be used in variable numbers, such as 2, 3
; OTHER INFORMATION: or 4 glycines.
; NAME/KEY: DISULFID
; LOCATION: (9)..(11)
; OTHER INFORMATION: cysteine residues may for example be involved in
; OTHER INFORMATION: bridge formation
; OTHER INFORMATION: Synthesised in Laboratory:
; OTHER INFORMATION: SDF-1(1-14)-(G)4-SDF-1(55-67)-C9/C11-cyclic acid
US-09-835-107-26

Query Match          100.0%; Score 175; DB 10; Length 31;
Best Local Similarity 100.0%; Pred. No. 4.9e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KPVSLSYRCPGRFFGGGLKWIQYLEKALN 31
Db      1 KPVSLSYRCPGRFFGGGLKWIQYLEKALN 31

RESULT 8
US-09-835-107-27
; Sequence 27, Application US/09835107
; Patent No. US20020165123A1
; GENERAL INFORMATION:
; APPLICANT: Tudan, Christopher R.
; APPLICANT: Merzouk, Ahmed
; APPLICANT: Arab, Lakhdar
; APPLICANT: Saxena, Geeta
; APPLICANT: Eaves, Connie J.
; APPLICANT: Cashman, Johanne
; APPLICANT: Clark-Lewis
; APPLICANT: Salari, Hassan
; TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS
; FILE REFERENCE: SMAR012
; CURRENT APPLICATION NUMBER: US/09/835,107
; CURRENT FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: CA 2,305,036
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/232,425
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: CA 2,335,109
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (15)..(18)
```

```
; OTHER INFORMATION: spacer monomers (such as the illustrated glycine
; OTHER INFORMATION: G's) may be used in variable numbers, such as 2, 3
; OTHER INFORMATION: or 4 glycines.
; NAME/KEY: DISULFID
; LOCATION: (9)..(11)
; OTHER INFORMATION: cysteine residues may for example be involved in
; OTHER INFORMATION: bridge formation.
; OTHER INFORMATION: Synthesised in Laboratory:
; OTHER INFORMATION: SDF-1(1-14)-(G)4-SDF-1(55-67)-C9/C11-cyclic amide
; NAME/KEY: MOD_RES
; LOCATION: (31)
; OTHER INFORMATION: AMIDATION
US-09-835-107-27
```

```
Query Match          100.0%; Score 175; DB 10; Length 31;
Best Local Similarity 100.0%; Pred. No. 4.9e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KPVSLSYRCPGRFFGGGLKWIQYLEKALN 31
Db      1 KPVSLSYRCPGRFFGGGLKWIQYLEKALN 31
```

```
RESULT 9
US-10-086-177A-13
; Sequence 13, Application US/10086177A
; Publication No. US20030148940A1
; GENERAL INFORMATION:
; APPLICANT: Tudan, Christopher R.
; APPLICANT: Merzouk, Ahmed
; APPLICANT: Saxena, Geeta
; APPLICANT: Eaves, Connie J.
; APPLICANT: Cashman, Johanne
; APPLICANT: Clark-Lewis, Ian
; APPLICANT: Salari, Hassan
; TITLE OF INVENTION: CXCR Agonist Treatment of Hematopoietic
; TITLE OF INVENTION: Cells
; FILE REFERENCE: SMAR-012CIP
; CURRENT APPLICATION NUMBER: US/10/086,177A
; CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: 09/835,107
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/232,425
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: CA 2,305,036
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: CA 2,335,109
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesised in Laboratory: SDF-1 (1-14) - (G)
US-10-086-177A-13
```

```
Query Match          100.0%; Score 175; DB 12; Length 31;
Best Local Similarity 100.0%; Pred. No. 4.9e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KPVSLSYRCPGRFFGGGLKWIQYLEKALN 31
Db      1 KPVSLSYRCPGRFFGGGLKWIQYLEKALN 31
```

```
RESULT 10
US-10-086-177A-15
; Sequence 15, Application US/10086177A
; Publication No. US20030148940A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Tudan, Christopher R.
; APPLICANT: Merzouk, Ahmed
; APPLICANT: Saxena, Geeta
; APPLICANT: Eaves, Connie J.
; APPLICANT: Cashman, Johanne
; APPLICANT: Clark-Lewis, Ian
; APPLICANT: Salari, Hassan
; TITLE OF INVENTION: CXCR Agonist Treatment of Hematopoietic
; FILE REFERENCE: SMAR-012CIP
; CURRENT APPLICATION NUMBER: US/10/086,177A
; PRIOR FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: 09/835,107
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/232,425
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: CA 2,305,036
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: CA 2,335,109
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized in Laboratory: SDF-1 (1-14) - (G)
; OTHER INFORMATION: 3-SDF-1 (55-67) amide: or CTCE0017
US-10-086-177A-15

Query Match      100.0%; Score 175; DB 12; Length 31;
Best Local Similarity 100.0%; Pred. No. 4.9e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KPVSLSYRCPCRFGGGGLKWIQYLEKALN 31
Db      1 KPVSLSYRCPCRFGGGGLKWIQYLEKALN 31

RESULT 11
US-10-086-177A-20
; Sequence 20, Application US/10086177A
; Publication No. US20030148940A1
; GENERAL INFORMATION:
; APPLICANT: Tudan, Christopher R.
; APPLICANT: Merzouk, Ahmed
; APPLICANT: Saxena, Geeta
; APPLICANT: Eaves, Connie J.
; APPLICANT: Cashman, Johanne
; APPLICANT: Clark-Lewis, Ian
; APPLICANT: Salari, Hassan
; TITLE OF INVENTION: CXCR Agonist Treatment of Hematopoietic
; FILE REFERENCE: SMAR-012CIP
; CURRENT APPLICATION NUMBER: US/10/086,177A
; CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: 09/835,107
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/232,425
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: CA 2,305,036
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: CA 2,335,109
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized in Laboratory: SDF-1 (1-14) - (G)
; OTHER INFORMATION: Synthesized in Laboratory: SDF-1 (1-14) - (G)
```

```
; OTHER INFORMATION: 4-SDF-1 (55-67) - E24/K28-cyclic acid
US-10-086-177A-20

Query Match      100.0%; Score 175; DB 12; Length 31;
Best Local Similarity 100.0%; Pred. No. 4.9e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KPVSLSYRCPCRFGGGGLKWIQYLEKALN 31
Db      1 KPVSLSYRCPCRFGGGGLKWIQYLEKALN 31

RESULT 12
US-10-086-177A-21
; Sequence 21, Application US/10086177A
; Publication No. US20030148940A1
; GENERAL INFORMATION:
; APPLICANT: Tudan, Christopher R.
; APPLICANT: Merzouk, Ahmed
; APPLICANT: Saxena, Geeta
; APPLICANT: Eaves, Connie J.
; APPLICANT: Cashman, Johanne
; APPLICANT: Clark-Lewis, Ian
; APPLICANT: Salari, Hassan
; TITLE OF INVENTION: CXCR Agonist Treatment of Hematopoietic
; FILE REFERENCE: SMAR-012CIP
; CURRENT APPLICATION NUMBER: US/10/086,177A
; CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: 09/835,107
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/232,425
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: CA 2,305,036
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: CA 2,335,109
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized in Laboratory: SDF-1 (1-14) - (G)
; OTHER INFORMATION: 4-SDF-1 (55-67) - K20/E24-cyclic acid
US-10-086-177A-21

Query Match      100.0%; Score 175; DB 12; Length 31;
Best Local Similarity 100.0%; Pred. No. 4.9e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KPVSLSYRCPCRFGGGGLKWIQYLEKALN 31
Db      1 KPVSLSYRCPCRFGGGGLKWIQYLEKALN 31

RESULT 13
US-10-086-177A-22
; Sequence 22, Application US/10086177A
; Publication No. US20030148940A1
; GENERAL INFORMATION:
; APPLICANT: Tudan, Christopher R.
; APPLICANT: Merzouk, Ahmed
; APPLICANT: Saxena, Geeta
; APPLICANT: Eaves, Connie J.
; APPLICANT: Cashman, Johanne
; APPLICANT: Clark-Lewis, Ian
; APPLICANT: Salari, Hassan
; TITLE OF INVENTION: CXCR Agonist Treatment of Hematopoietic
; FILE REFERENCE: SMAR-012CIP
; CURRENT APPLICATION NUMBER: US/10/086,177A
```

```

; CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: 09/835,107
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/232,425
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: CA 2,305,036
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: CA 2,335,109
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized in Laboratory: SDF-1 (1-14) - (G)
; OTHER INFORMATION: 4-SDF-1 (55-67) - E24/K28-cyclic acid: or CTCE0022
US-10-086-177A-22
```

```

Query Match          100.0%; Score 175; DB 12; Length 31;
Best Local Similarity 100.0%; Pred. No. 4.9e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KPVSLSYRCPCRFEGGGGLKWIQEYLEKALN 31
Db      1 KPVSLSYRCPCRFEGGGGLKWIQEYLEKALN 31
```

```

RESULT 14
US-10-086-177A-23
; Sequence 23, Application US/10086177A
; Publication No. US20030148940A1
; GENERAL INFORMATION:
; APPLICANT: Tudan, Christopher R.
; APPLICANT: Merzouk, Ahmed
; APPLICANT: Saxena, Geeta
; APPLICANT: Eaves, Connie J.
; APPLICANT: Cashman, Johanne
; APPLICANT: Clark-Lewis, Ian
; APPLICANT: Salari, Hassan
; TITLE OF INVENTION: CXCR Agonist Treatment of Hematopoietic
; TITLE OF INVENTION: Cells
; FILE REFERENCE: SMAR-012CIP
; CURRENT APPLICATION NUMBER: US/10/086,177A
; CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: 09/835,107
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/232,425
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: CA 2,305,036
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: CA 2,335,109
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized in Laboratory: SDF-1 (1-14) - (G)
; OTHER INFORMATION: 4-SDF-1 (55-67) - K20/E24-cyclic acid: or CTCE0021
US-10-086-177A-23
```

```

Query Match          100.0%; Score 175; DB 12; Length 31;
Best Local Similarity 100.0%; Pred. No. 4.9e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KPVSLSYRCPCRFEGGGGLKWIQEYLEKALN 31
Db      1 KPVSLSYRCPCRFEGGGGLKWIQEYLEKALN 31
```

```

RESULT 15
US-10-086-177A-26
; Sequence 26, Application US/10086177A
; Publication No. US20030148940A1
; GENERAL INFORMATION:
; APPLICANT: Tudan, Christopher R.
; APPLICANT: Merzouk, Ahmed
; APPLICANT: Saxena, Geeta
; APPLICANT: Eaves, Connie J.
; APPLICANT: Cashman, Johanne
; APPLICANT: Clark-Lewis, Ian
; APPLICANT: Salari, Hassan
; TITLE OF INVENTION: CXCR Agonist Treatment of Hematopoietic
; TITLE OF INVENTION: Cells
; FILE REFERENCE: SMAR-012CIP
; CURRENT APPLICATION NUMBER: US/10/086,177A
; CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: 09/835,107
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/232,425
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: CA 2,305,036
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: CA 2,335,109
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized in Laboratory: SDF-1 (1-14) - (G)
; OTHER INFORMATION: 4-SDF-1 (55-67) - C9/C11-cyclic acid
US-10-086-177A-26
```

```

Query Match          100.0%; Score 175; DB 12; Length 31;
Best Local Similarity 100.0%; Pred. No. 4.9e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KPVSLSYRCPCRFEGGGGLKWIQEYLEKALN 31
Db      1 KPVSLSYRCPCRFEGGGGLKWIQEYLEKALN 31
```

Search completed: October 9, 2003, 09:28:28
Job time : 375 secs